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Scoring table:

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The present sequence is mouse Stat3 protein fragment containing 1-154 amino acids of Stat3 protein. This Stat3 fragment showed very weak binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Stat3-c-Jun interaction region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse Stat3 protein fragment #1 (1-154 amino acids).
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/note= "N-terminal domain"
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ABU04735
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ABU04743
ADH57035
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ADN04464
AAU84356
AAR41334
ABU04740
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AAW03168
AAW62994
AAB19962
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                                                                                                                                                                                                                                                                                    ABP98871
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Zhang X, Horvath C,
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WO200116605-A2
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AAY72840;
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                                                                                                                                                                                          MAQWNQLQQLDTRYLKQLHQ.....AVVTEKQQMLEQHLQDVRKR 154
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Compugen Ltd.
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Copyright (c) 1993 - 2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339 -40) were cloned in plasmids 13sfl and 19sf6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                  Signal transduder and activator of transcription; STAT; 19sf6; Stat3; receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor recognition: factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                                     LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                             1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
  transformation; These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain; linker domain, SH2 domain and transactivation domain
                                                                                                                           1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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                                                                                 tch al Similarity 100.0%; Score 800; DB 4; al Similarity 100.0%; Pred. No. 1.1e-77; 154; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                     AAR72082 standard; protein; 770 AA
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94US-00212184.
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N-PSDB; AAQ89340.
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Best Local Similarity
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11-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse signal transducer and activator of transcription (STAT) protein STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also DNA binding in a receptor recognition and message delivery vi DNA binding domains (see also AAW03167) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and
                                                                                                                                                           1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAT; STAT4; signal transducer and activator of transcription; DNA binding protein; ligand; receptor; oncogenesis; inflammation; autoimmune disease; antagonist; therapy.
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                                               Length 770;
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100.0%; Pred. No. 9e-77;
Mismarches 0;
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/label= DNA binding domain
/note= "Claim 3, page 110"
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Sequence 770 AA;
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Example; Col 47-50; 44pp; English
      Disclosure; Fig 1; 42pp; English
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                                                                                                                                                                                                                                                                                                                       Murine STAT3 protein.
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                                                                                                  61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                          1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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                                                                                                                                                                                                                                         , signal transducer and activator of transcription, crystal, design, murine.
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                              Length 770;
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/label= 3(10) helix of alpha helix 2
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                                                                                                                         121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                 STAT-3 protein.
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/label= Alpha helix 3
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activation of transcription
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The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of grater than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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         signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural compound that binds to the N-terminal domain of a STAT protein.

Compound that binds to the N-terminal domain of a STAT protein, identifying a compound that enhances or diminishes the binding of the dimeric STAT proteins to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter containing at least two adjacent weak binding sites of a promoter of a gene containing at least two adjacent weak binding sites of a for STAT protein dimers. The methods are used for identifying new drugs. An antagonist of STAT N-terminal dimeric interactions that inhibits the binding of the STAT dimers to adjacent weak binding sites on diseases, e.g. inflammation, allery, asthma and lenkaemias. On the other hand, an agonist of N-terminal dimeric interactions between STAT dimers, can be used as drugs in the treatment of diseases e.g. anneamia, neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and growth retardation. The present sequence is murine STAT3 protein
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  for detecting compounds that bind to
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/note= "Residues 79, 83, 86, 90 and 94 contribute to
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77. .96
//label= alpha helix 7
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/label= alpha_helix_3
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| Jabel= alpha_helix_4
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 invention relates to methods
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Best Local Similarity
Matches 154; Conserv
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transducer and activator of transcription (STAT) protein, where the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the N-terminal domain of the STAT protein to a resolution of greater than 5.0 Angstrom. The methods and compositions are useful for the design and screening of drugs that enhance or inhibit STAT-STAT dimeninteractions. The present sequence represents the amino acid sequence of mouse STAT3 protein
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100.0%; Pred. No. 9e-77;
ive 0; Mismatches 0;
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/label= alpha_helix_8
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24-APR-2000; 2000US-00556273.
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KURIYAN J.
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Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator Sjogren's syndrome, multiple sclerosis, Addison's disease, epilepsy, polymyositis, rheumatoid arthritis, autoimmune infertility, anaemia, proliferative disease, Grave's disease, ulcerative colitis, sarcoma, carcinoma; degenerative disorder, gene therapy, growth deficiency; cirrhosis, hypoproliferative disorder, lesion; Statbeta. 713. .714 /note= "Encoded by ACA CCA TTC" Disclosure; Page 87-89; 94pp; English Dalton W; Location/Qualifiers 08-SEP-2000; 2000US-0231212P 10-SEP-2001; 2001WO-US028254 Jove R, UNIV JOHNS HOPKINS UNIV SOUTH FLORIDA 2002-362218/39. Misc-difference 713 transcription 3. Pardoll D, N-PSDB; AAD35066. WO200220032-A1 Homo sapiens 14-MAR-2002 ( OCXI) (UYSF-) Yu H, \$\frac{1}{2}\$\frac

The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing, bypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chonic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a syndrom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, signature syndrome, scleroderma, polymyostitis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirthosis, permitious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, victuling, gluten-sensitive enteropathy, autoimmune butropenia myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, victuling, autoimmune cinfertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating appearing a specific proliferative and oncedenic disease which includes sarcomas and conversioners. carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3beta protein

Sequence 720 AA;

Gaps ö Length 720; 0; Indels DB 5; Score 792; DB 5; Pred. No. 6e-76; 2; Mismatches 99.0%; Matches 152; Conservative Similarity Query Match Local

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1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL

Mouse ischaemic condition related protein sequence SEQ ID NO:398 Mouse, ischaemia, compressive ischaemia, occlusive ischaemia, vasospastic ischaemia, ischaemic condition, ischaemic disease TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154 Ź ABB57164 standard; protein; 769 18-MAY-2000; 2000JP-00145977. 18-MAY-2001; 2001WO-JP004192 (first entry) WO200188188-A2 Mus musculus. 07-MAR-2002 22-NOV-2001 61 121 121 ABB57164; 61 RESULT 셤 Db ઠે

. occlusive ischemia) by measuring defined in the specification or by Examining the ischemic condition (e.g. occlusive ischemia) by measur expression levels of particular genes defined in the specification determining the expression profile of a gene group comprising these Ishii Y; Takahashi Y, Nagata T, Asai S, WPI; 2002-034733/04. N-PSDB; ABI99454 Ishikawa K, genes.

(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON

Claim 2; Page 1084-1087; 2690pp; English.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB5734) or by determining the protein sequences in ABB57020 to ABB5734) or by determining the levels or expression profile of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or primars for a mouse ischaemic diseases. AB199913 and AB199914 represent PCR primars for a mouse ischaemic tondition related sequence, which are used in the exemplification of the present invention

Sequence 769 AA;

ö 1 MAGWNOLOOLDTRYLKOLHOLYSDTFPMELROFLAPWIESQDWAYAASKESHATLVFHNL Gaps . 0 Length 769; 0; Indels 99.0%; Score 792; DB 5; 98.7%; Pred. No. 6.5e-76; ive 2; Mismatches 0; Conservative Query Match Best Local Similarity Matches 152;

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us-10-090-185-8.rag

myasthenia gravis,

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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stati). Modulating angiogenesis is useful for treating or preventing thypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, crisum ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for amplicating a symptom of an autoimmune disease such as systemic lupus extrementosus, multiple sclerosis, insulin dependent diabetes mellitus, siggren's syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                                                                          immune response; Stati; cornary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; solymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; epilopsy polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; disease; ulcerative colitis; sarcoma; carcinoma; degenerative discoder; gene therapy; growth deficiency; cirrhosis; hypoproliferative discoder; lesion.
                                                                                                                                                                                                                                                                                                                                                                                           Human; signal transducer and activator of transcription 3; ischaemia,
                                                                     154
                                                                                       TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                   TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR
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                                                                                                                                                                                                                  AAE22054 standard; protein; 769 AA
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                                                                                                                                                                                                                                                                                                                                                  Human Stat3 protein.
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                    idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoad lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and earthomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 769;
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Pred. No. 6.5e-76;
2; Mismatches 0;
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SOUTH FLORIDA.
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Best Local Similarity 98.7
Matches 152; Conservative
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(UYSF-) UNIV
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transfucer and activator of transcription 3 (Stata). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, rauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, ofronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, introgen necroasis, proliferative angiopathy e.g. diabetic microangiopathy epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, or introgen necroasis, proliferative aniongpathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, signate on autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, allower enteropathy, autoimmune neutropenia, mysethenia gravis, idiopathic thromboxycopenia purpura, Grave's disease, coodpestures and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, chence deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, thypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human construction related to angiogenesis regulation
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compound that modulates the activity of a signal transducer and activator
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Pred. No. 6.5e-76;
2; Mismatches 0; Indels
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                                                                       Disclosure; Page 83-85; 94pp; English
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98.7%;
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; acute phase response factor; transcription factor; interleukin-6;
                                                                                                                                                                New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
                                                                                                                                                                                                                                                         The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (I 6). The protein is encoded by a CDNA, isolated from a mouse liver CDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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                                                                                                                                                                                                                                                                                                                                                                 inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 792; DB 2; Length 77
Pred. No. 6.5e-76;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human placenta acute phase response factor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR82993 standard; protein; 770 AA
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Best Local Similarity 98.7%;
Matches 152; Conservative
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                                                                                        Akira S, Kishimoto T;
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                                                          (KISH/) KISHIMOTO T.
                                                                                                                    WPI; 1995-346089/45
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    hypertension, etc
                                                                                                                                      N-PSDB; AAT05619
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 770 AA;
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                               04-APR-1994;
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29-MAR-1995;
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Length 770; Indels 9 9

diseases

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The present sequence represents a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. The encoding sequence differs from the original published human STAT3 gene sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3 protein is useful as a medicament or pharmaceutical composition for treatment of autoimmune or inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                  LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                 99.0%; Score 792; DB 2; L 98.7%; Pred. No. 6.5e-76; ive 2; Mismatches 0;
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Best Local Similarity 98.7
Matches 152; Conservative
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                                                                                                                                                                       The sequence corresponds to a human acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is expressed from a human placenta cDNA, isolated using an IL-6-treated mouse liver cDNA probe. APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer,
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98.7%; Pred. No. 6.5e-76;
iive 2; Mismatches 0,
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                                                                                                                                                                                                                                                                                        osteoclasia, pulmonary hypertension, etc
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                                                                                                                                         Claim 3; Page 9-12; 31pp; English
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Matches 152; Conservative
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               1995-346089/45.
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N-PSDB; AAT05616
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WPI; 2001-101568/11. N-PSDB; AAA89229.

Claim 2; Page 9-13; 32pp; English

disease

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transcription 3 (STAT-3). The invention provides a crystal of a core portion of a STAT protein in dimer form with an 18-mer duplex DNA (see AAA89233) that contains a binding site for the STAT dimer. The core portion comprises a coiled-coil domain comprising 4 long helices, a DNA binding domain which contains an immunoglobulin-like fold, a C-terminal STAT protein an immunoglobulin-like fold, a C-terminal crystal is of sufficient quality to perform X-ray crystallography studies. Methods of preparing the crystals are included in the invention. Knowledge of the STAT protein's 3-dimensional structure will aid in structure-based drug design. The crystal can be used in drug screening assays to identify agonist and antagonist compounds. Antagonists can be used to treat inflammation, allergy, asthma and leukaemia, and agonists to treat anaemia, neutropenia, thrombocytopenia, cancer, obesity, viral diseases, growth retardation, and other conditions characterized by insufficient STAT activity
                                                                                                                                              present sequence is that of human signal transducer and activator of
Novel crystal useful in drug screening assays, comprises portion of signal transducer, activator of transcription and duplex DNA.
                                                                                  Disclosure; Col 67-71; 206pp; English
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invention

Sequence 770 AA;

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LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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Query Match 99.0%; Score 792; DB 4; Length 770; Best Local Similarity 98.7%; Pred. No. 6.5e-76; Matches 152; Conservative 2; Mismatches 0; Indels
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ABG69497 standard; protein; 770 AA (first entry) Human bait protein STAT3. 21-OCT-2002 Homo sapiens ABG69497; RESULT 15 ABG69497 

Human, yeast two-hybrid assay, adipocyte, bait protein, NIDDM, non-insulin diabetes mellitus, obesity, selected interacting domain, SID, protein-protein interaction map, PIM, anorectic, metabolic disorder.

WO200253726-A2.

11-JUL-2002.

28-DEC-2001; 2001WO-EP015423

02-JAN-2001; 2001US-0259377P

(HYBR-) HYBRIGENICS. (CNRS ) CENT NAT RECH SCI

Jockers R; Legrain P; Marullo S,

WPI; 2002 583612/62 N-PSDB; ABS51033

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The invention relates to a complex of protein-protein interactions

(forming a protein-protein interaction map, PIM) in adipocyte cells as

defined in the specification, or polynucleotides in adipocyte sencoding

for the polypeptides. Also included are a recombinant cell expressing the

interacting polypeptides and a method of selecting a modulating compound

in adipocyte cells, by cultivating a recombinant host cell on a selective

medium containing a modulating compound and a reporter gene the

expression of which is toxic for the recombinant host cell which is

transformed with two vectors, where the first vector comprises a

coplynucleotide encoding a first hybrid polypeptide and DNA binding domain

and the second vector comprising a polynucleotide encoding a second

hybrid polypeptide and an activating domain that activates the toxic

creporter gene, when the first and second hybrid polypeptides interact and

selecting the modulating compound which inhibits the growth of the

creombinant host cell (i.e. using the yeast two-hybrid system). The

complexes are useful for identifying compounds that modulate the protein-

compound isolated by the method is useful for treating and preventing

compound isolated by the method is useful for treating and preventing

compound isolated by the method is useful for treating and preventing

cobsenty or metabolic diseases. The interactions between the proteins of

the complex further define a set of selected interacting admains, SID.

The present sequence represents a member of the protein complex of the

invention, used as the bait protein in the yeast two-hybrid assay
Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders.
                                                                                                                              Claim 1; Page 54; 125pp; English
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Length 770; 0; Indels Score 792; DB 5; Pred. No. 6.5e-76; 2; Mismatches 0. 99.0%; Query Match Best Local Similarity 98.77 Matches 152, Conservative

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Gaps .; 0 9

61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 1 MAQWNOLOQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60 --ઠ g à 셤

1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL

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5, 2005, 15:01:09 Job time : 50.8306 secs completed: May Search

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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-956-869-12

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US-09-1364-970-3

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US-09-136-12

US-09-136-12

US-08-110-12

US-08-110-12

US-08-110-12

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US-08-110-12

US-08-110-12

US-08-110-12

US-09-17-087-12

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US-09-17-087-12

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US-09-17-087-12

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Maximum Match 100%
Listing first 45 summaries
                                           - protein search, using sw model
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length: 2000000000
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380
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120

TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154 121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154

121

1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL LGEIDQQYSRFLQESNVLYQHURRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA

MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL

100.0%; Score 800; DB 3; Length 154; 100.0%; Pred. No. 7.3e-79; ive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 154; Conservative

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g ò g APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Zhong Zhong
APPLICANT: Zhong Zhong
TITLE OF INVENTION: TRANSDUCER AND ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS

; Sequence 12, Application US/08369796; Patent No. 5716622; GENERAL INFORMATION:

US-08-369-796-12

RESULT 2

999	Seguence 6, Appli Seguence 6, Appli	9	~	Sequence 6, Appli	12,	12,	4	4,	4	4,	4,	4	~	Sequence 1, Appli	ORS OF TRANSCRIPTIONAL ACTIVATOR		
	US-08-948-547-6 US-08-956-653A-6		_	PCT-US95-17025-6	_	_			_	_	_	_	_	US-09-364-970-1	ULT 1 09-387-418A-8 equence 8, Application US/09387418A equence No. 6391572 ENERAL INDORMATION: APPLICANT: Zhang, Xiaokui APPLICANT: The Correct No. Curt M APPLICANT: Darnell Jr., James E TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS FILE REFERENCE: 600-1-253 CURRENT APPLICATION NUMBER: US/09/387,418A CURRENT FILING DATE: 1999-08-31 CURRENT FILING DATE: 1999-08-31 SOFTWARE: PATENTIN Ver. 2.0 SOFTWARE: PATENTIN Ver. 2.0 FILE REPORT OF STATES STA		
	712 3 712 3			712 5	740 1									750 3	SULT 1  -09-387-418A-8 Sequence 8, Application US/09387418A Patent No. 6391572 GENERAL INFORMATION: APPLICANT: Zhang, Xiaokui APPLICANT: Zhang, Xiaokui APPLICANT: Arzeszczynska, Melissa i APPLICANT: Horvath, Curt M APPLICANT: Horvath, Curt M APPLICANT: Darnell Jr., James E TITLE OF INVENTION: METHODS FOR ID TITLE OF INVENTION: METHODS FOR ID TITLE OF INVENTION: INTERACTIONS FILE REPERENCE: 600-1-253 CURRENT APPLICATION NUMBER: US/09/3 CURRENT PELILOGIONS: 43 SOFTWARE: PatentIN Ver. 2.0 SEQ ID NO 8		
47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5		47.5	Application US/ 3391572 3391572 3391572 Shang, Xiaokui Wreaszczynska, Wreaszczynska, Wreaszczynska, Wreyath, Curt Darnell Jr., J VEWTION: INTER NCE: 600-1-253 LIGATION NUMBER LIG DATE: 1995 Patentin Ver. 2		
380	380 380	380	380	380	380	380	380	380	380	380	380	380	380	380	SULT 1 -09-387-418A-8 Sequence 8, Application US/ Batent No. 6391572 GENERAL INFORMATION: APPLICANT: Zhang, Xiaokui APPLICANT: Wrzeszzynska, APPLICANT: Mrzeszzynska, APPLICANT: Darnell Jr., J TITLE OF INVENTION: METHO TITLE OF INVENTION: INTERFERENCE: 600-1-25 FLLE REFERENCE: 600-1-25 CURRENT APPLICATION NUMBER CURRE	TYPE: PRT	 
28	30 31	32	33	3.4 4.4	36	3.7	38	39	40	41	42	43	44	45	RESULT 1 US-09-387-418A-8 Sequence 8, Ap Batent No. 639 GENERAL INFORM APPLICANT: Z APPLICANT: W APPLICANT: D TITLE OF INVE TITLE OF INVE FILE REPERRIC CURRENT PEPLI CURRENT FILIN NUMBER OF SEQ SOFTWARE: Pa SEQ ID NO 8 SEQ ID NO 8 SECTION OF	, TYPE	

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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
FILING DATE: 11-MAR-1994
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                  FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26.742
REFERENCE/DOCKET NUMBER: 600-1-116
                                                                UMBER: US/08/852,091
06-MAY-1997
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SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 201 487-5800
TELEX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 154; Conservative
                                     CURRENT APPLICATION DATA APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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Patent No. 588328
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Curt M. Horvath
APPLICANT: Curt M. Horvath
APPLICANT: Trans Zilong Zilong Zilong Trans Zilong Zilon
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                                                                                                                                                                                                                                                                               COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/POCKET UNMBER: 600-1-116
TELEPHONE: 201 487-5800
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COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"OWDITER: IBM PC COMpatible
"OWDITER: TOWN PC COMPATIBLE
                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
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Matches 154; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                           CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
   NUMBER OF SEQUENCES:
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STATE: New Jersey
COUNTRY: USA
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Sequence 12, Application US/0895652

Patent No. 6013475

GENERAL INFORMATION:

APPLICANT: Schindler, Christian W. APPLICANT: Fu, Xian-Yuan

APPLICANT: Fu, Xian-Yuan

APPLICANT: The Xian-Yuan

APPLICANT: Application W. Zilong

TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackro-

STREET: 411 Harth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                                                                                                                   NAME: Jackson Esg., David A.
REGISTATION UNDBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHOXE: 201 343-1684
TELER: 133521
                 FILING DATE: 23-NOV-1992
FRICING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
FRICING DATE: 19-WAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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AUDRESS:
LIRET: Klauber & Jackson
LIRET: 411 Hackensack Avenue
CITY: Hackensack Avenue
STATE: New Jersey
COUNTRY: USA
COUNTRY: USA
WPIPP: 0760'
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 133521
INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
APPLICATION NUMBER: US 07
FILING DATE: 23-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-820-754-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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Fatent No. 6030808;
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James B.,
APPLICANT: Schindler, Christian W.,
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: REQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCES: 25
CORRESPONDENCES: 25
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 800; DB 3; Length 770; Best Local Similarity 100.0%; Pred. No. 5.9e-78; Matches 154; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                   APPLICATION NUMBER: US US/11/185
FILING DATE: 11-WAR.1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR.1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 08/126,588
FILING DATE: 19-WAR.1993
APPRORNEY/AGENT INFORMATION:
NAME: JACKSON ESQ., David A.
REGISTRATION NUMBER: 26,742
FELERENCE/DOCKET NUMBER: 2
US 08/212,185
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USA
APPLICATION NUMBER
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PAPPLICATION NUMBER: US/08/948,547
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US/07/980,498
FILING DATE: 23-NOV-1992
                                                                                                              26,742
PP· 600-1-194
  APPLICATION NUMBER: US/09/012,710
                 FILING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKEY NUMBER: 600-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
TELERA: 1335-1
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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Patent No. 6124118
GENERAL INFORMATION:
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STREET: 411 Hackensack Avenue
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STATE: New Jersey
COUNTRY: USA
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MOLECULE TYPE:
HYPOTHETICAL: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
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APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: William of Moarefi, James E.
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                       APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
RIONG APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
RION APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
APPLICATION NUMBER: US/08/956,869
                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/212,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09012710 Patent No. 6087478
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 13321
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-956-869-12
                                                                                                                FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07601
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMBIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                        1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                                                                               1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Query Match 100.0%; Score 800; DB 3; Length 770; Best Local Similarity 100.0%; Pred. No. 5.9e-78; Matches 154; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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FILING DATE:
CLASSIFICATION:
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                                                                                                                     -09-364-970-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: UNSFROLIFERATIVE CELLULARORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT PILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                             NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                         FILING DATE: 19-WAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
US 07/854,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09364970 Patent No. 6235873
                                                                                                                                                                                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-948-547-12
  APPLICATION NUMBER:
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ORGANISM: Mus musculus
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TELEX: 13
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Best Local
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                                                                        APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT PILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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APPLICANT: Vinkemeier, Uwe
APPLICANT: Warrefi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Darnell, Jr., James E.
APPLICANT: Ruriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 770;
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100.0%; Pred. No. 5.9e-78;
iive 0; Mismatches 0;
121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                             121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
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APPLICATION NUMBER: US/09/556,273
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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APPLICATION NUMBER: 09/012,710
FILING DATE:
                                                                                                                                                                                           Sequence 5, Application US/09364970 Patent No. 6235873
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Best Local Similarity 100.0
Matches 154; Conservative
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; ORGANISM: Mus musculus
US-09-364-970-5
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                  Length 770;
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ADDRESSEE: Klauber & Jackers STREET: 411 Hander & Jackers
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 800; DB 3;
100.0%; Pred. No. 5.9e-78;
ive 0; Mismatches 0;
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION WUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
RPLICATION WUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
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CITY: Hackensack
                                                                                                                                           TELEX: 133521
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
ATTORNEY/AGENT INFORMATION NAME: Jackson Esq., Davi
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 154; Conservative
                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
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LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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5.9e-78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
PAPLICATION NUMBE: US/08/212,185
FILING DATE: 11-MAR-1994
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100.0%; Score 800; D
Best Local Similarity 100.0%; Pred. No. 5.9
Matches 154; Conservative 0; Mismatches
               FILING DATE: 19-MAR-1993
RICAN APPLICATION DATA:
PAPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATORNEY/AGENT INFORMATION:
NAME: Jackson Bsq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-195
TELECOMMUNICATION INFORMATION:
TELECHONE: 201 343-1684
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WO US93/02569
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APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR PELICATION DATA:
APPLICATION NUMBER: US 07/854,296
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 660542
GENERAL INFORMATION:
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STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                              : 770 amino acids
amino acid
                                                                                                                                                                                                                                                                                               TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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, MOLECULE TYPE: protein US-08-416-581B-1
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ZIP: 20037
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APPLICANT: Jilong Wen
APPLICANT: Cutr M. Horvath
APPLICANT: Cutr M. Horvath
APPLICANT: Cutr M. Horvath
APPLICANT: Chong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STREET: 411 Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 · LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
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ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 800; DB 4;
Pred. No. 5.9e-78;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 101604
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GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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100.0%;
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                                                                                                                                                                                                                                                                  TELEX: 13351
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-212-185-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-17025-12
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAQWNQLQQLDTRYLKQLHQLYSDTFPWELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAQWNQLQQLDTRYLKQLHQLYSDTPPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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                                                                                                                                                                                                                                                                                                                                               100.0%; Score 800; DB 5; Length 770; 100.0%; Pred. No. 5.9e-78; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flam PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
PRIOR APPLICATION 1435
PRIOR APPLICATION WHERE: JP 6-65825/1994
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08416581B
Patent No. 5719042
GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-37891
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 600-
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEFAX: 133221
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 770 amino acids TYPE: amino acids TYPE: amino acids TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (202) 293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                MOLECULE TYPE: protein PCT-US95-17025-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Query Match
99.0%; Score 792; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 4.3e-77;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps
ON 1 MADWANDIOGRAPHY CONTERNATION PROPERTY.
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0;	09	120
0; Gaps	VEHNL             VFHNL	LOTAA         LOTAA
0;	ESHATI        ESHATI	WEESRI 
Indels	ODWAYAASKU           QDWAYAASKU	IARIVARCLI          IARIVARCLI
Ö	PWIES	EKPME 
nservative 2; Mismatches 0	SDTFPMELRQFLA   :         SDSFPMELRQFLA	LRRIKQFLQSRYL              LRRIKQFLQSRYL
2,	HOLY	NHOY:
itches 152; Conservative 2; Mismatches 0; Indels	1 MAGWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLABWIESQDWAYAASKESHATLVFHNL 60	61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 
152;	1 MA(	61 LG 
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Search completed: May 5, 2005, 14:58:51 Job time: 26.1906 secs

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5, 2005, 14:59:00 ; Search time 64.8612 Seconds (without alignments) 792.064 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAQWNQLQQLDTRYLKQLHQ.....AVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: \( \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO7} \\ \text{PUBCOMB.ppp:*} \)

2: \( \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO5} \\ \text{NEW} \\ \text{PUB.ppp:*} \)

3: \( \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO6} \\ \text{NEW} \\ \text{PUB.ppp:*} \)

4: \( \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO6} \\ \text{NEW} \\ \text{PUB.ppp:*} \\ \text{pp:*} \\ \text{cgn2} \( 6/\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO6} \\ \text{NEW} \\ \text{PUB.ppp:*} \\ \text{pp:*} \\ \text{cgn2} \( 6/\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO8} \\ \text{NEW} \\ \text{PUB.pp:*} \\ \text{pp:*} \\ \text{cgn2} \( 6/\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO9} \\ \text{PUBCOMB.ppp:*} \\ \text{11:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO9} \\ \text{PUBCOMB.ppp:*} \\ \text{12:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO9} \\ \text{PUBCOMB.ppp:*} \\ \text{13:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO9} \\ \text{PUBCOMB.ppp:*} \\ \text{13:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO9} \\ \text{PUBCOMB.ppp:*} \\ \text{14:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO9} \\ \text{PUBCOMB.ppp:*} \\ \text{15:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USO0} \\ \text{PUBCOMB.ppp:*} \\ \text{16:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USOO} \\ \text{PUBCOMB.ppp:*} \\ \text{16:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USIOD} \\ \text{PUBCOMB.ppp:*} \\ \text{16:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USIOD} \\ \text{PUBCOMB.ppp:*} \\ \text{16:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpaa} \\ \text{USIOD} \\ \text{PUBCOMB.ppp:*} \\ \text{16:} \\ \cgn2 \frac{6}\) \text{prodata} \( 2/\) \text{pubpa} \\ \text{USOOD} \\ \text{PUBCOMB.ppp:*} \\ \t
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1428581 seqs, 333598853 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%,
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                      May
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Sequence 8, Appli	Sequence 12, Appl	Sequence 8, Appli	Sequence 12, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 56, Appl	Sequence 2, Appli	Sequence 329, App	Sequence 349, App	Sequence 780, App	Sequence 780, App	
) 1 ( ) 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	τD	US-10-090-185-8	US-09-876-773-12	US-10-045-792-8	US-10-639-617-12	US-10-380-020-4	US-10-380-020-2	US-10-380-020-5	US-10-038-010-56	US-10-117-087-2	US-10-116-275-329	US-10-116-275-349	US-09-925-302-780	US-09-925-302-780	
	DB	13	11	14	11	15	15	15	14	14	15	15	6	10	
	% Query Match Length DB	154	770	770	770	720	769	769	770	770	770	770	793	793	
	% Query Match	100.0	100.0	100.0	100.0	99.0	99.0	99.0	99.0	99.0	99.0	0.66	99.0	0.66	
	Score	800	800	800	800	792	792	792	792	792	792	792	792	792	
	Result No.	п	~	m	4	2	9	7	ω	o	10	11	12	13	

Seguence 11, Appl	6, A	'n	9	m	'n	Sequence 4, Appli	_	44,	352,	823,	19, A	4, A	Sequence 550, App	Sequence 4, Appli	Sequence 6, Appli	Sequence 8, Appli	7	Sequence 39, Appl	Sequence 8, Appli	Seguence 4, Appli	Sequence 10, Appl	10,	٥,	437	439,	70,	362,	389	Seguence 2, Appli	Sequence 2, Appli	Sequence 2, Appli
13 US-10-090-185-11	11 US-09-876-773-6	14 US-10-245-120-2	17 US-10-639-617-6	17 US-10-936-390-5	9 US-09-833-205-2	11 US-09-876-773-4	14 US-10-245-120-1	14 US-10-308-279-44	16 US-10-755-889-352	16 US-10-755-889-823	17 US-10-492-043-19	17 US-10-639-617-4	9 US-09-925-297-550	9 US-09-833-205-4	9 US-09-833-205-6	11 US-09-876-773-8	4	14 US-10-205-194-39	17 US-10-639-617-8	14 US-10-245-120-4	11 US-09-876-773-10	17 US-10-639-617-10	14 US-10-045-792-9	US-10-177	14 US-10-177-293-439	16 US-10-755-889-70	16 US-10-755-889-362	14 US-10-205-823-389	11 US-09-876-773-2	14 US-10-045-792-2	15 US-10-179-451-2
154	712	712	712	712	750	750	750	750	750	750	750	750	786	749	749	749	749	749	749	131	748	748	749	423	748	748	748	532	851	851	851
47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.2	47.2	47.2	47.2	47.2	47.2	45.0	41.8	41.8	41.8	41.7	41.7	41.7	41.7	30.9	30.9	30.9	30.9
380	380	380	380	380	380	380	380	380	380	380	380	380	380	378	378	378	378	378	378	360	334.5	334.5	334.5	333.5	333.5	333.5	333.5	247.5	247.5	247.5	247.5
14	15	16	. 17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

APPLICANT: Zhang, Xiaokui
APPLICANT: Mrzeszczynska, Melissa H
APPLICANT: Mrzeszczynska,
APPLICANT: Mrzeszczynska,
APPLICANT: Mrzeszczynska,
APPLICANT: Mrzeszczynska,
APPLICANT: Mrzeszczynska,
APPLICANT: Darnell Jr., James
TITLE OF INVENTION: MRTHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR F
TITLE OF INVENTION: MRTHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR F
FILE REFERENCE: 600-1-253
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET. 2.0 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 9 9 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 0; Gaps 100.0%; Score 800; DB 13; Length 154; 100.0%; Pred. No. 4.7e-77; tive 0; Mismatches 0; Indels 0; Sequence 8, Application US/10090185 Publication No. US20020197647A1 GENERAL INFORMATION: Query Match Best Local Similarity 100. Matches 154; Conservative TYPE: PRT
CORGANISM: Mus musculus
US-10-090-185-8 JS-10-090-185-8 g ð g ò

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121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                     121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-045-792-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAQWNQLQQLDTRYLKQLHQLYSDTFPWELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
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                                                                                                                                                                                                                                                                               Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/212,185

RILING DATE: 11-MAR-1994

APPLICATION NUMBER: US 07/980,498

FILING DATE: 23-NOV-1992

APPLICATION NUMBER: US 07/854,296

FILING DATE: 19-MAR-1992

APPLICATION NUMBER: US 07/854,296

FILING DATE: 19-MAR-1993

APPLICATION NUMBER: US 08/126,588

FILING DATE: 19-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 800; DB 11;
100.0%; Pred. No. 3.7e-76;
iive 0; Mismatches 0;
                       TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12
                                                                                                      RESULI 4
US-09-876-773-12
i Sequence 12, Application US/09876773
i Publication No. US20040058318A1
i GENERAL INFORMATION:
i APPLICANT: Darnell Jr., James E.
i Fu, Xian-Yuan
Fu, Xian-Yuan
                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                  Wen, Zilong
Zhong, Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 154; Conservative
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Best Local Similarity
121
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                     Moarefi, Ismail
Darnell, Jr., James E.
Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                  4th Floor
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ATTORNEY/AGENT INFERMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-0ct-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue,
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SEQUENCE DESCRIPTION: SEQ ID NO: 8:
78-10-045-792-8

Sequence 8, Application US/10045792

Publication No. US20030003563A1

GENERAL INFORMATION:

APPLICANT: Vinkemeier, Uwe
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TELEFAX: 201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
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INFORMATION FOR SEQ ID NO:
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Pred. No. 2.4e-75;
2; Mismatches 0;
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Pred. No. 2.7e-75;
2; Mismatches 0;
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Best Local Similarity 98.7%;
Matches 152; Conservative
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Best Local Similarity 98.7%;
Matches 152; Conservative
                                                                   Sequence 4, Application US/1036
Publication No. US20040052762A1
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ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                           Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEI.
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 4.35
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
FILING DATE: 11-MAR-1994
FILING DATE: 13-MOV-1992
APPLICATION NUMBER: US 07/886,496
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESC, DAVIG A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
THE DATE OF THE PROPERTY OF THE P
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100.0%; Pred. No. 3.7e-76;
ive 0; Mismatches 0;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                     Sequence 12, Application US/10639617
Publication No. US20050079543A1
GENERAL INPORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Klauber & Jackson
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: 201 343-1684
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SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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Best Local Similarity 100.
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 133521
-10-639-617-12
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APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Pardoll, Drew
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-019-9990
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 720 APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Pardoll, Drew
APPLICANT: Dave, Richard
APPLICANT: Dave, Richard
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Version 3.0
SEQ ID NO 2
LENGTH: 769 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 9 1 MAQWNQLQQLDTRYLEQLHQLYSDSFFWELRQFLAPWIESQDWAYAASKESHATLVFHNL 60 1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL Gaps Gaps .. 0 ö Length 769; Length 720; ò

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ORGANISM: Human
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US-10-117-087-2
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                                                                                                                                                                                                                                    APPLICANT: Yu, Hua
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Daton, Willian
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REPERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: 2003-07
PRIOR PLING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
61 LGBIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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Fublication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
SEC ID NO 56
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Pred. No. 2.7e-75;
2; Mismatches 0;
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                                                                              121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                   Sequence 5, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
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Matches 152; Conservative
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ORGANISM: Homo Sapiens
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LENGTH: 769
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APPLICANT: 0'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Brayden, Daragh
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
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Score 792; DB 14; Length 770; Pred. No. 2.7e-75; 2; Mismatches 0; Indels
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APPLICANT: SERLUFI-CRESCENZI, Ottaviano
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
FILE REFERENCE: SERLUFI=2
CURRENT APPLICATION NUMBER: US/10/117,087
CURRENT RILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US/09/526,542
PRIOR APPLICATION NUMBER: US/09/526,542
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.0
SEQ ID NO 2: LENGTH: 770
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Pred. No. 2.7e-75;
2; Mismatches 0;
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Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Blan Pharmaceutical Technology
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Publication No. US20030166854A1
GENERAL INFORMATION:
Query Match
Best Local Similarity 98.7%;
Matches 152; Conservative
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Best Local Similarity 98.7%;
Matches 152; Conservative
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Pred. No. 2.8e-75;
2; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                 Length 793;
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAION: Nucleic Acids, Proteins and Antibodies CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: CT/US00/05918
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                              Query Match
99.0%; Score 792; DB 9; L
Best Local Similarity 98.7%; Pred. No. 2.8e-75;
Matches 152; Conservative 2; Mismatches 0;
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 780
LENGTH: 793
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; Sequence 780, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
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; Sequence 11, Application US/10090185
; Publication No. US20020197647A1
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Best Local Similarity 98.7%;
Matches 152; Conservative
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US-09-925-302-780
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US-09-925-302-780
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LENGTH: 793
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APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Hambkin, Imelda
APPLICANT: Higgins, Liea
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and Mcells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILLING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 349
LENGTH: 770
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99.0%; Score 792; DB 15; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                            Length 770;
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Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
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ORGANISM: Homo sapiens
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US-09-925-302-780
                                                         TYPE: PRT
ORGANISM: Rat
US-10-116-275-329
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     SEQ ID NO 329
LENGTH: 770
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                                                                                        FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bsg., David A.
REGISTRATION NUMBER: 26, 742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
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                              FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
APPLICATION NUMBER: WO US93/02569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-876-773-6
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                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 712 amino acids
                                                                                                                                                                                                                                                                                                                            TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                completed: May !
le : 65.8612 secs
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Job time :
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                                                                              APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James B
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR I
TITLE OF INVENTION: INTERACTION:
TITLE OF INVENTION: INTERACTION: INTERACTION:
TITLE OF INVENTION: INTERACTION:
TITLE OF INVENTION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
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TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 380; DB 13;
; Pred. No. 2.5e-32;
42; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 23 NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09876773
Publication No. US2004058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian Yuan
Wen, Zilong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 411 Hackensack Avenue
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ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                      Wrzeszczynska, Melissa H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.88;
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69; Conservative
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                       Zhang, Xiaokui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 69; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07601
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1;

Gaps 2;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

5, 2005, 14:55:35; Search time 11.2329 Seconds (without alignments) 1319.101 Million cell updates/sec May Run on:

US-10-090-185-8

800 1 MAQWNQLQQLDTRYLKQLHQ......AVVTEKQQMLEQHLQDVRKR 154 Perfect score: Sequence:

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

į		*			SUMMARIES		
Result No.	Score	Query Match	Query Match Length	DB	ID.	Description	
:	792	,	770	~	A5444	DNA-binding prote	61.
7	792		770	7	149508	ω	ש
٣	380	47.	739	7	A46159	interferon-depende	de
4	334.5	41.	748	7	A56047	gamma-interferon	ಥ
S	247.5		851	7	A46160	interferon alpha-i	·~
9	188		786	0	149274	mammary gland fact	ct
7	187		794	7	G02317		ţį
80	186		793	~	S54772	mammary gland fact	Ċţ
6	147.5		794	0	S55527		ct
10	96		331	7	AI0354	probable lipoprote	te
11	97		837	7	157557		ei
12	91.5		848	7	A54740	interleukin-4-indu	фŋ
13	88	11.0	1355	7	T22552	hypothetical prote	te
14	82.5	10.3	371	7	T40287	cal	te
15	82.5	10.3	373	~	F71884		λs
16	82	10.2	498	7	C69587	L-arabinose isomer	er
17	82	10.2	620	7	856790	probable membrane	Ð
18	82	10.2	764	ď	C83513	hypothetical prote	t e
19	81.5	10.2	276	~	H81707	inclusion membrane	пe
50	81	10.1	2954	~	T14156	æ	pr
21	80.5	10.1	1110	~	A43253	Large tra-1 protei	ei.
22	80	10.0	508	Н	KRSHL2	keratin type II,	E
23	79.5	9.9	392	N	T19867	<ul> <li>hypothetical prote</li> </ul>	te
24	79.5	9.9	444	~	E90192	DNA repair protein	in
25	79.5	9.9	613	~	S48557	hypothetical pro	te
56	79.5	9.9	638	~	153169	cytokeratin 2 -	- hu
27	79.5	9.9	4957	~	T03455		Щà
28	79.5	9.9	5262	~	34		ma
53	79	9.9	4540	~	T30838	<ul> <li>cytoplasmic dynein</li> </ul>	in

A19508
ISGR3 p91-related transcription factor - mouse
ISGR3 p91-related transcription factor - mouse
ISGR3 p91-related transcription factor - mouse
C;Species: Nus musculus (house mouse)
C;Dacession: 149508; I49009
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tra A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: I49508
A;Status: preliminary; translated from GB/EMBL/DDBJ

MG328 homolog P01_	nuclear mitotic ap	ninein - mouse	hypothetical prote	keratin, 65K type	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	probable transcrip	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	probable alpha-act	probable alpha-act
873693	A42184	T30171	F71956	A29666	T00345	T30637	AB2247	T20241	T37604	A72108	B86514	C83192	T34180	T13414	T13413
7	7	7	7	~	~	7	~	7	~	~	7	7	7	~	7
1033	2101	2168	409	629	1462	2133	191	2160	625	390	390	442	812	895	924
9.8	9.8	9.6	9.6	9.8	9. 8.	9.7	9.6	9.6	9.6	9.5	9.5	9.5	9.5	9.4	9.4
78.5	78.5	78.5	78	78	78	77.5	77	77	76.5	9/	9/	9/	92	75.5	75.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1

1	
. AS4444	
DNA-binding protein APRF - human	
C;Species: Homo sapiens (man)	
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004	text_change 09-Jul-2004
C,Accession: A54444	
R,Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka,	S.; Matsusaka, T.; Yoshida, K.; Sud
Cell 77, 63-71, 1994	ļ
A, Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3	ulated gene factor 3 p91-related tra-
A;Reference number: A54444; MUID:94208062; PMID:7512451	451
A; Accession: A54444	
A;Status: preliminary; translated from GB/EMBL/DDBJ	
A; Molecule type: mRNA	
A; Residues: 1-770 eRES>	000 - 010 -
A) CLOSSE' CELECICES: ONLERCI: F40/05; GB:L636/1; N1D:G4/07/09; F1D:G4/07/09	10/00/ FID:91/0/09
A.Comicinos	
A.COLLE. ADD. LALV.	
1. troughtion 17421-1740	
rings boarton. Thimso signs I transducer and transcription artivator STATSA	tion activator STATSA
C;Keywords: DNA binding; transcription factor	
99.0%; Score 792; DB 2;	Length 770;
BESC LOCAL SIMILATICY 98./*; FIEC. NO. I.IE-01; Nataboom 150. Consequenting Nataboom 0. Indels	
132; Combervacive 2; mismacches 0;	THE COLD
Qy 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL	ESQDWAYAASKESHATLVFHNL 60
Db 1 MAQMNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL	
Qy 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWRESRLLQTAA	MEJARIVARCI, WEESRLLOTAA 120
Db 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLBKPMEIARIVARCLWEESRLLQTAA	
OV 121 TAAOOGGOANHPTAAVVTEKOOMLEOHLODVRKR 154	
Db 121 TAAQQGGQANHPTAAVVTBKQQMLEQHLQDVRKR 154	

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Query Match
Best Local Similarity
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A;Residues: 1-851 <YAN>
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     C; Accession: A56047
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Matches
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A;Residues: 1-770 <RES>
A;Cross-references: UNTROT:P42227; GB:L29278; NID:g476715; PIDN:AAA37254.1; PID:g476716
A;Cross-references: UNTROT:P42227; GB:L29278; NID:g476715; PIDN:AAA37254.1; PID:g476716
B;Az, R.; Durbin, J. B.; Levy, D. B.
J. Biol. Chem. 269, 24391-24395, 1994
A;Fitle: Acute phase response factor and additional members of the interferon-stimulated A;Reference number: 149009; MUID:95014185; PMID:7523373
A;Accession: 149009
A;Accession: I49009
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Accelletype: mRNA
A;Residues: 1-393, M', 395-700, 702-770 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 21.56p-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C; Date: 21.56p-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C; Date: 21.56p-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C; Schindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A; Fiteference number: A46159; MUID:92366557; PMID:1502203
A; Accession: A46159
A; Accession: A46159
A; Molecule type: nucleic acid; protein
A; Residues: 1-739 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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C,Species: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAQWINGLOOLDTRYLKOLHOLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890 C;Genetics: A;Gene: APRF C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Cross-references: UNIPROT: P42224
A, Experimental source: HeLa cella
A, Note: sequence extracted from NCBI backbone (NCBIP:110818)
C, Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                 Length 770
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.5%; Score 380; DB 2;
ilarity 44.8%; Pred. No. 1.5e-25;
Conservative 42; Mismatches 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Score 792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 152; Conservative
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69; Conserv
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A;Title: The genomic structure of the STAT genes: multiple exons in coincider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NyAlternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
Proc. Natl. Acad. Sci. Us. A. 89, 7840-7843, 1992
A;Ftu X. Y; Schindler, C.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. Us. A. 89, 7840-7843, 1992
A;Fitle: The proteins of ISGF-3, the interferon alpha-induced transcriptions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interferon alpha-induced transcription activator ISGR-3, 113K chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAQWNQLQQLDTRYLKQLHQLYSDTFPWELRQFLAPWIESQDWAYAASKESHATLVFHNL
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37.6%; Pred. No. 7.5e-14;
live 34; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 41.8%; Score 334.5; DB 2; Similarity 41.4%; Pred. No. 1.5e-21; 63; Conservative 38; Mismatches 50;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN-A
A;Cross-references: UNIPROT: P42229; EMBL: U43185; NID:g1151169; PIDN:AAB06589.1; PID:g115
C;Superfamily: human signal transducer and transcription activator STATSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
E;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
EMBO J. 14, 1166-1175
EMBO J. 14, 11
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A;Modecule type: mRNA
A;Residues: 1-793 <MUI>
A;Residues: 1-793 <MUI>
A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:Z48538; NID:g758633; PIDN:CAA88
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stats and an additional homologue (Stat5b) involved in Arreference number: 149273; MUID:96004632; PMID:7568026
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                                                                                                                                                                                                                                                                                                                                                                        23.4%; Score 187; DB 2; Length 794; 31.4%; Pred. No. 1.4e-08;
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llarity 29.5%; Pred. No. 1.7e-08;
Conservative 26; Mismatches 76,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQ 149
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                                          Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 31.4%; Pred. No. 1.4e-48; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: stat5 protein
                                          Data
                                                                            A;Reference number: H01043
A;Accession: G02317
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A; Residues: 1-793 <RES>
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           R;Lin, J:
submitted to the EMBL
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Best Local Simi
Matches 46;
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Best Local
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A;Molecule type: mRNA
A;Residues: 1-78 G.KES.
A;Cross-references: UNIPROT: P42232; UNIPROT: 09JKM1; EMBL: U21110; NID: 9747973; PIDN: AAC52
B;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
B;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A;Reference number: S54772; MUID: 95237198; PMID: 7720707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-432, 'E', 434-786 <MUI>
A;Cross-references: EMBL:Z48839; NID:g758635; PIDN:CAA88420.1; PID:g758636
B;Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris, A;Title: Interleukin-3 signals through multiple isoforms of Stat5.
A;Reference number: S54725; MUID:95246733; PMID:7537213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Niviteriate names: STATS protein homolog p80
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149274; S54773; S54772
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Rytitle: Cloning and expression of Stats and an additional homologue (Stat5b) involved: A;Reference number: 149273; MUID:96004632; PMID:7568026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                               61 FHFLDQLNYECGRCSQDPESLLLQHNLRKFCRDIQP-FSQDPTQLAEMIFNLLLEEKRIL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 FHNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LEGLVQELQKKAEHQVGEDGFLLKIKLGHYATQLQSTYDRCPMELVRCIRHILYNEQRLV 120
                                                                                                                                                     HNLLGEIDQQYSRFLQE-SNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLL 116
transcription activator stat5A - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 786;
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                                                                                                                                                                                                                                                                                                   117 QTAATAAQQGGQANHPTAAVVTEKQQ-MLEQHLQDVR 152
                                                                                                                                                                                                                                                                                                                                                                     120 IQAQRAQLEQGE---PVLETPVESQQHEIESRILDLR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 QTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REANNGSSPAGS----LADAMSQKHLQINQTFEELR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.5%; Score 188; DB 2; ilarity 30.1%; Pred. No. 1.1e-08; Conservative 26; Mismatches 75;
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A;Residues: 1-432,'E',434-786 <AZA>
C;Genetics:
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les 47; Conserve
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R;Quelle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M..; Clevel, Mol. Cell. Biol. 15, 3336-3343, 1995
Mol. Cell. Biol. 15, 3336-3343, 1995
A;Title: Cloning of murine Stat6 and human Stat6, Stat proteins that are tyrosine phosphol A;Reference number: I57557; WUID:95280934; PMID:7760829
A;Accession: 157557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-837 <RES>
A;Cross-references: UNIPROT:P52633; GB:L47650; NID:g1008876; PIDN:AAA79006.1; PID:g100887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
187 NL-----LDTTRKLENLTDIERQLSSRKQLQNEIPETDAEAKSAAEAKSAENQPAAAKPA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-Binding Protein and transcription factor - mouse C;Species: Wus musculus (house mouse) C;Species: Way-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004 C;Accession: IS7557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGEIDQQYSRFLQE---SNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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A;Residues: 1-848 <HOU>
C;Superfamily: human signal transducer and transcription activator STATSA C;Reywords: DNA binding: transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Superfamily: human signal transducer and transcription activator STATSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 265, 1701-1706, 1994
A,Title: An interleukin-4-induced transcription factor: IL-4 stat.
A,Reference number: A54740, MUID:94367369; PMID:8085155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 12.1%; Score 97; DB 2
Best Local Similarity 24.8%; Pred. No. 1.2;
Matches 29; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 LEKPMEIARIVARCLWEESRL-
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Best Local Similarity
'-hes 43; Conserva
                                                          139 EKQ 141
                                                                                                               242 ESK 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics
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C;Species: Yersinia pestis
C;Species: Yersinia pestis,
C;Accession: A10354
Requence revision 02-Nov-2001
Reparkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Reparkhill, J.; Wren, B.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Altitle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q8ZCQ6; GB:AL590842; PIDN:CAC92164.1; PID:g15980878; GSPDB:d
                                                                                    C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S55527; 84433
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corriganda. Mammary gland factor (MGF) is a novel member of the cytokine regula A;Accession: S55527; MUID:95188889; PMID:7882987
                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g6023 A;Cross-references: UniproT: the sequence from reference S44353 B;Wakao, H.; Gouilleux, F.; Groner, B. EMBO J. 13, 2182-2191, 1994 A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcrible A;Reference number: S44353; MUID:94244619; PMID:7514531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 YSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQQYSRFLQESNVLYQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYA----ASKESHATLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 FHNLLGEIDQQYSRFLQESNVLYQHNL-RRIKQFLQSRYLEKPMEIARIVARCLWEESRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reaidues: 17-716, RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 794;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.4%; Score 147.5; DB 2; Length 27.3%; Pred. No. 4.1e-05; ive 27; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::|::|::|
----GNSSAGILVD--AMSQKHLQ 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>..</del>
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VREATN----
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                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-794 < WAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: AI0354
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
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Best Local S:
Matches 36
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51; Gaps

Indels

57;

31; Mismatches

96

-LRRIKOFLOSRYLE--

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206 G----YPRGTKNSFKATIFEKNEDPDYIVEGVWTGESKLTIPSLKSTIFFLSIPSLEAT 260
                                                                                                                                                                                                                                                                            261 PITVKPESEMGDWESRNVWKE-----VSAALASGNYD-----IVSSKKSTIEQSQRDM 308
                                                                                                                                                                                                                                            97 ----KP-MEIARIVARCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDV 151
                                                  5 NQLQQLDTRYLKQLHQLYSDTFP---MELRQFLAPWIESQDWAYAASKESHATLVFHNLL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: May 5, 2005, 15:01:50
Job time : 18.2329 secs
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                                                                                                                                               62 GEIDQQYSRFLQES -- NVLYQHN-
     44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <ARN>
                                                                                                                                                                                                                                                                                                                                           152 RKR 154
                                                                                                                                                                                                                                                                                                                                                                                         RKK 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1355 <WIL>
A;Cross-references: EMBL:292788; PIDN:CAB07214.1; GSPDB:GN00019; CESP:ZK1151.1
A;Experimental source: clone F53B8
R;Harris, B.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z20408
A;Accession: T27703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA.
A;Residues: 1-1355 <MIZ>
A;Cross-references: EMBL:293398; PIDN:CAB07724.1; GSPDB:GN00019; CESP:ZK1151.1
A;Experimental source: clone ZK1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             737 QW----DWILLALSKCLEEHLRDALNLKSFMEEASDA-EAWIQEQSVRLENNYNRTDFSLE 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -------35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SPBC354.07c - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40287
R;Wood, V; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A. A;Reference number: 221918
A;Reference number: 221918
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-371 <WOO>
                                                                                                                                                              hypothetical protein ZK1151.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dacte: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T22552; T27703
R;Harris, B.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19580
A;Accession: T22552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Andecus: preliminary; translated from A;Accession: T2552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SRYLEKPMEIARIVARCLWEESRLLQTAATAA---QQGGQANHP 132
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133 TAAVVTEKOOMLEOHLOD 150
                                          168 TPANGTGPSEALAMLLOE 185
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Matches 42; Conservative
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A;Gene: CESP:ZK1151.1
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A,Cross-references: EMBL:AL022071; PIDN:CAA17807.1; GSPDB:GN00067; SPDB:SPBC354.07c A,Experimental source: strain 972h-; cosmid c354

A;Gene: SPDB:SPBC354.07c

A; Map position: 2 A; Introns: 8/2; 75/3

Score.82.5; DB 2; Length 371; Pred. No. 8.4;

10.3%;

Query Match Best Local Similarity

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C;Accession: F71884
A;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Isham, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path, A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: F71884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:092KW4; GB:AE001511; GB:AE001439; NID:g4155382; PIDN:AAD0639
A;Experimental source: strain J99
probable lipopolysaccharide biosynthesis protein - Helicobacter pylori (strain J99)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 LHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQQYSRFLQESNV 77
                        C.Species: Helicobacter pylori
A,Variety: strain J99
C.Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.3%; Score 82.5; DB 2; Length 373; Best Local Similarity 33.8%; Pred. No. 8.4; Matches 27; Conservative 14; Mismatches 26; Indels 13
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5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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OM protein - protein search, using sw model

Мау Run on:

5, 2005, 14:55:35 ; Search time 41.6706 Seconds (without alignments) 1892.467 Million cell updates/sec

US-10-090-185-8

1 MAQWNQLQQLDTRYLKQLHQ.....AVVTEKQQMLEQHLQDVRKR 154 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

1612378 Total number of hits satisfying chosen parameters:

1612378 segs, 512079187 residues

Searched:

length: 0 length: 2000000000 seq DB DB Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	P40763 homo sapien	P42227 mus musculu	P52631 rattus norv	P61635 bos taurus	Q6dv79 gallus gall	Q9pvx8 xenopus lae	Q7zxk3 xenopus lae		_	093599 brachydanio				Q90y16 tetraodon f	O8jgn0 xenopus lae	P42224 homo sapien	Q68d00 homo sapien		ratt	mus	mus	mus	Q8c497 mus musculu	Q9d323 mus musculu	Q9qxk0 rattus norv	Q8c8m3 mus musculu	Q764m5 sus scrofa	Q90y17 tetraodon f	013132 oncorhynchu	O13131 oncorhynchu	Q801y2 carassius a
ID	STA3 HUMAN	STA3 MOUSE	STA3_RAT	STA3 BOVIN	Q6DV79	Q9PVX8	Q7ZXK3	Q7ZTS5	Q6NV46	093599	013133	Q6DVF3	Q6GUE7	Q90Y16	Q8JGN0	STA1_HUMAN	Q68D00	Q6P6Q7	Q7TP57	Q99K94	STA1_MOUSE	Q8C3V4	Q8C497	Q9D323	оэржко	Q8C8M3	Q764M5	Q90Y17	013132	013131	Q801Y2
DB		Н	ч	Н	~	~	~	~	~	~	~	~	N	~	~	Н	7	N	N	7	ч	~	~	7	7	~	~	~	~	7	7
Length	770	770	770	770	771	169	166	414	786	908	767	765	785	764	751	750	750	712	1165	712	749	749	749	749	749	755	757	758	754	754	718
% Query Match	99.0	99.0	0.66	98.2	97.4	95.0	93.6	86.8	86.8	86.8	86.4	85.7	85.7	85.2	50.1	47.5	47.5	47.4	47.4	47.2	47.2	47.2	47.2	47.2	47.2	47.2	47.2	44.3	43.9	43.2	42.1
Score	792	792	792	786	779	760	749	694.5	694.5	694.5	691.5	685.5	685.5	681.5	401	380	380	379	379	378	378	378	378	378	378	378	378	354.5	351	346	336.5
Result No.		8	e	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

093598 brachydanio 06p943 brachydanio P4228 mus musculu 014765 homo sapien 066hb2 rattus norv 07227 brachydanio 08aw20 brachydanio 072253 brachydanio 0801x2 brachydanio 0801y2 brachydanio 0801y2 brachydanio 080415 tetraodon f 090y15 tetraodon f
093598 06P943 26P943 STA4 MOUSE STA4 HUMAN 066HB2 02Z277 08AW24 08AW24 08AW20 0803U9 0803U9 0807U8 0807U8
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336.5 334.5 333.5 333.5 331.5
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# ALIGNMENTS

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TISSUBERIGE FROM N.A. (ISOFORMS 1 AND DEL-701).

TISSUBERIdney, and Pancreas;

MEDLINEE-2138825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
Yoshida K., Sudo T., Naruto M., Kishimoto T.;
"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
Rajkumar N., Yi Q., Nickerson D.A.;
"SeattleSNPs. NHLBI HL6682 program for genomic applications, UW-
FHCRC, Seattle, WA (URL: http://pga.gs.washingron.edu).";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
"Highly conserved amino-acid sequence between murine STAT3 and a
revised human STAT3 sequence.";
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
STA3 HUMAN STANDARD; PRT; 770 AA.
P40763; 014916; Q9BW54;
01-FEB-1995 (Rel. 31, Created)
05-UUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                             Name=STAT3; Synonyms=APRF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathway.";
Cell 77:63-71(1994).
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                  response factor)
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STA3 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0005737; C:cytoplasm; TAS.
GO:0005634; C:nucleus; TAS.
GO:0005602; F:hematopoietin/interferon-class (D200-domain. .; TAS.
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I. Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coactivator NCOA/SRCIa.";
J. Biol. Chem. 277:8004-8011(2002)
-!- FUNCTION: Transcription factor that binds to the interleukin-6
-(IL-6)-responsive elements identified in the promoters of various acute-phase protein genes.
-!- PATHWAY: Involved in the gp130-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI.
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
                                                                                                                                                                                                                                                                                                                                MEDLINE=95215843; PubMed=7701321;
Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
"Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11773079; DOI=10.1074/jbc.M111486200;
Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
"Functional interaction of STAT3 transcription factor with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOJG-P40761-2; Sequence-VSP 010474;
ISOJG-P40765-2; Sequence-VSP 010474;
TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.

PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, ILF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.

SIMILARITY: Belongs to the transcription factor STAT family.

SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                            Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P40763-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ012463; CAA10032.1; -. EMBL; AY572796; AA866966.1; -. EMBL; BC000627; AAH00627.1; -. EMBL; BC014482; AAH14482.1; -. EMBL; AF029311; AAB84254.1; -.
                                                                                                                                                                                                 SEQUENCE OF 564-704 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L29277; AAA58374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     Science 267:1990-1994(1995)
                                                                                                                                  and mouse cDNA sequences.'
                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION ON SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:11364; STAT3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERACTION WITH NCOAL
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HSSP; P42227; 1BG1.
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                                                                                                                                                                                                                        rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                      complexes."
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                                                                            ., TAS
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MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;.
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
Yoshida K., Sudo T., Naruto M., Kishimoto T.;
"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphotyrosine (by JAK) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
                                                                                                                                                                                                                                                                                                                                               Activator; Alternative splicing; DNA-binding; Nuclear protein;
Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
DOMAIN S80 670
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last amnotation update)
Signal transducer and activator of transcription 3 (Acute-phase
  Fitranscription factor activity, TAS.
P:cell motility, TAS.
P:JAK-STAT cascade, TAS.
P:negative regulation of transcription from P.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphoserine (By similarity)
Missing (in isoform Del-701).
/FIId=VSP 010474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 792; DB 1; Length 770; Pred. No. 7.3e-60; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q -> K (in dbsNP:1803125).
/FTId=VAR_018683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6C00632211C8012D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O -> H (in Ref. 1)
P -> S (in Ref. 1)
K -> N (in Ref. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F -> Y (in Ref. 1)
V -> L (in Ref. 1)
T -> A (in Ref. 1)
GO, GO:0003700; F:transcription factor activit GO; GO:0006928; P:cell motility; TAS. GO; GO:000728; P:cell motility; TAS. GO; GO:000122; P:negative regulation of trans GO; GO:0007399; P:neurogenesis; TAS. GO; GO:0007399; P:neurogenesis; TAS. InterPro; IPR009967; PS3_like_DNA_bnd. InterPro; IPR009980; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR 018679
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88067 MW;
                                                                                                                                                                                                                     Pfam; PF0017; ST2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF0264; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
PROSITE; PS50001; SF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.7%;
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Stat3; Synonyms=Aprf;
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                                                                                                                                                                                                                                                                                                                                                                                                                            705
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460
548
561
667
730
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730
770 AA;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenco L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,

B Diatcherco M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahe, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rohing M., Kazaywinski M.I., Skalska U., Smailus D.E.,

B Butterfield Y. S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                  MEDLINE=95014185; PubMed=7523373;
Raz R., Durbin J.E., Levy D.E.;
"Acute phase response factor and additional members of the interferonstimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
                                                                               Zhong Z., Wen Z., Darnell J.E. Jr., "Stat1: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6."; Science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.
MEDLINE-59354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
WHEN Z., Zhong Z., Darnell J. E. C.
"Maximal activation of transcription by Stat1 and Stat3 requires both
                                                                                                                                                                                                                                                                                                                                   Schaefer T.S., Sanders L.K., Nathans D.; "Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J, and NOD/LtJ;
Davoodi.Semiromi A., She J.-X.;
"A mutant Stat5b with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
MEDLINE=96016116; Pubmed=7568080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine and serine phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM STAT3A).
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM STAT3A).
                                          SEQUENCE FROM N.A. (ISOFORM STAT3A)
                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM STAT3A)
                                                             TISSUE=111ymus,
MEDLINE=94188718; PubMed=8140422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 71:150-155(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
pathway.";
Cell 77:63-71(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zebrafish to mouse.";
                                                                                                                                                                                                                                                                                                                                                                 Stat3.";
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129/SvJ;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                            -i-FUNCTION: Transcription factor that binds to the interleukin-6
-i-FUNCTION: Transcription factor that binds to the interleukin-6
-i-FUNCTION: Transcription genes STAT3B interacts with the N-terminal acute-phase protein genes STAT3B interacts with the N-terminal part of JUN to activate such promoters in a cooperative way.
-i-PATHWAY: Involved in the gp130-mediated signaling pathway.
-i-SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).
-i-SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name-Del-701;
Isole P42227-3; Sequence=VSP 010475;
Isole P42227-3; Sequence=VSP 010475;
Isole P42227-3; Sequence=VSP 010475;
Isole P42227-3; Sequence=VSP 010475;
Isole SPECIFICITY: STAT3A is geen in the liver, although in a much less abundant manner.
Isole Specific Section of Section 1.6, IL-11, CNTF, ILF, CSF-1, EGF, FDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodymes and maximal transcriptional activity (By similarity).
Isole Section Section 1.6 Section 1.6 Section 1.6 STAT Family.
Isole Section 1.6 Section 1.6 Section 1.6 STAT Family.
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GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005864; C:plasma membrane; IDA.
GO; GO:0005865; C:plasma membrane; IDA.
GO; GO:0005515; F:DNA binding; IDI.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007259; P:JAK-STAT cascade; IDA.
GO; GO:0007259; P:JAK-STAT cascade; IDA.
GO; GO:0006357; P:regulation of transcription from Pol II pro. .
InterPro; IPR008967; P53_like_DNA_bnd.
X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
MEDLINE-98334373; PubMed=9671298; DOI=10.1038/28101;
Becker S., Groner B., Mueller C.W.;
"Three-dimensional structure of the Stat3beta homodimer bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3D-structure; Activator; Acute phase; Alternative splicing; Direct protein sequencing; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P42227-2; Sequence=VSP_006287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P42227-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in response to phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U06922; AAA19452.1; --
EMBL, U08370; AAA56668.1; --
EMBL, U30709; AAC52612.1; --
EMBL, AF29489; AAL59017.1; --
EMBL; AY29489; AAC75418.1; --
EMBL; AY29490; AAC75418.1; --
EMBL; BC003806; AAH03806.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L29278; AAA37254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; 149508; 149508.
PDB; 1BG1; X-ray; A=1-722.
TRANSFAC; T01574; -.
MGD; MGI:103038; Stat3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001217; STAT.
                                                                                                                                                                                                              Nature 394:145-151(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50001; SHZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02865; STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Stat3A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Stat3B;
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FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various
 Biol. Chem. 270:29998-30006(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STA3 BOVIN
P61635;
                                                                                                                                                                                                                                                                                                                                                      MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Transcription factors Stat3 and Stat5b are present in rat liver nuclei late in an acute phase response and bind interleukin-6 response
                  Phosphotyrosine (by JAK) (By similarity).
                                    TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
                                                                                                                                                                                                                                                                                                                                                              1 MAQWNOLQOLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                              MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                             FDMDLTSECATSPM -> FIDAVWK (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998; Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                          S->A: Decreased transcriptional
                                                                                                                                                                                                                                                                                                           Length 770;
                                                                     Missing (In isoform Del-701). /FTId=VSP_010475.
                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                         E -> K (in Ref. 2).
S -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
 Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
Name=Stat3;
                                                                                                                                                                                                                                                                                                          99.0%; Score 792; DB 1;
98.7%; Pred. No. 7.3e-60;
iive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                               FTId=VSP_006287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   770 AA.
                                                                                                  activation.
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SH2 domain;
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.7°
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                 705
                                                                       701
                                                                                        727
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TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
Phosphorylation;
          580
705
727
716
                                                                       701
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STA3_RAT
ID STA3_RAT
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MOD_RES
MOD_RES
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                                                                       VARSPLIC
                                                                                        MUTAGEN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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acute-phase protein genes.
-!- PATHWAY: Involved in the gp130-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).
-!- PTM: Tyrosine phosphorylation (By similarity).
-!- PTM: Tyrosine phosphorylation of Similarity.
-!- FTM: Tyrosine phosphorylation of stable DNA-binding STAT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF012864; STAT alpha; 1.
Pfam; PF028665; STAT int; 1.
SMART; SM00252; SH2; 1.
PROSITE; PSSC001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          705 705 Phosphotyrosine (by JAK) (By similarity) 727 727 Phosphoserine (By similarity). 770 AA; 88039 MW; D74AQC76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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                                                                                                                                                                                                                                                                                                                                  homodimers and maximal transcriptional activity (By similarity). SIMILARITY: Belongs to the transcription factor STAT family. SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Signal transducer and activator of transcription 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (6 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X91810; CAA62920.1; -.
HSSP; P42227; 1BG1.
RGD; 3772; Stats.
InterPro; IPR00980; F53_like_DNA_bnd.
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
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05-JUL-2004 (Rel. 44, Last seq
25-OCT-2004 (Rel. 45, Last ann
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Les 152; Conserv
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TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                   TAAQQGGQATHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=stat 3;
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       embryos independent of BMP-4.";
Dev. B101. 1216:481-490(1999).
EMBL; ABO17701; BAA866061.1; --
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02865; STAT_bind; 1.
Pfam; PF02865; STAT_lit; 1.
SWART; SW00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                            Best Local Similarity 96.8
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae, Xenopus.
NCBI_TaxID=8355,
                                                                                                                                               PROSITE, PS50001; SH2
SEQUENCE 771 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stat 3
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                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                      61 LGEIDOOYSRFLOESNVLYOHNLRRIKOFLOSRYLEKPMEIARIVARCLWEESRLLOTAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQLLAPWIESQDWAYAASKESHATLVFHNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50001; SH2; 1. Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphotyrosine (by JAK) (By
Phosphoserine (By similarity)
9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou G.Y., Leung F.C.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; ANG441397; ANG468B71; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 786; DB 1;
Pred. No. 2.4e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAQOGGOANHPTAAVVTEKOOMLEOHLODVRKR 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ620655; CAF06182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           705 705 PP
727 727 PP
770 AA; 87974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAGWNQLQQLDTRYLEQLHQLYGDSFPMELRQFLAPWIESQDWAYAANKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518; Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T., Asashima M., Yokota T.; "Activation of Stat3 by cytokine receptor gpl30 ventralizes Xenopus
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000967; SF3_like_DNA_bnd.
InterPro; IPR001217; STAT.
Pfam; PF0017; STAT.
Pfam; PF0017; STAT_alpha; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005634, C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; P53 like_DNA_bnd.
InterPro; IPR00980; SHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                             771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50001; SH2; 1.
769 AA; 87974 MW; 0905C03263303069 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          97.4%; Score 779; DB 2; Le
96.8%; Pred. No. 9.7e-59;
....ematches 2;
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InterPro;
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                                                        InterPro,
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                     LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                            9
                       MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                        MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAFAASKESHATLVFHNL
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GO:0004871; F:signal transducer activity; IEA.
GO:0004870; F:transcription factor activity; IEA.
GO:0007242; P:transcription factor activity; IEA.
GO:0007342; P:intracellular signaling cascade; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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MEDLINE22241132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC044717; AAH44717.1; -.
HSSP; P42227; 1BG1.
GO; GO:0005434; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007700; F:transcription factor activity; IEA.
GO; GO:0007742; P:intracellular signaling cascade; IEA.
GO; GO:000555; P:equlation of transcription, DNA-depen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                          TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                        766 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stat3-A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=stat3-A;
                                                                                                                                        61
                                                                                                                                                                                           19
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Q7ZXK3
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ERQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TRAINAB; TISSUE-Whole body;

RX MINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Mary D.M., Sodergren B.J., Lu X., Glubs R.A.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Mary, Some M.S., Scheren B.J., Lu X., Glubs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Ratkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Ratkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Razywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

M. Jones S.J., Marra M.A., Palley S., Schein J.E.,

Janes S.J., Marra M.A., Stalska U., Smallus D.E., Schnerch A., Schein J.E.,

Janes B.J., Marra M.A., Stalska U., Smallus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSTYLEKPMBIARIVARCLWEEGRLLQTAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAFAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAQWNOLQOLDTRYLKOLHOLYSDTFPMELROFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
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                                                                                                                                                                                                                                                                                                                                               87599 MW; 31018A3321CCEB9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%; Score 749; DB 2; L
92.2%; Pred. No. 3.7e-56;
live 6; Mismatches 6;
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P53_like_DNA bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                               Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02865; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequences.
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                                           IPR000980;
IPR001217;
                                                                                                                                                                                                                                                                                                                                                           766 AA;
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NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 142;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Cypriniformes;
ZFIN; ZDB-GENE-980526-68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR00967; F33 like_DNA_bnd.
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                                                                                                                                                                                                                                                                                                                   DB 2; Length 414;
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Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                     Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
SEQUENCE 414 AA; 48253 MW; OPFD1B509B7526BD CRC64;
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                                                                                                                                                                                                                                                                                                                     86.8%;
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Matches 133; Conservative
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Name=stat3;
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Q6NV46
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LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii; Teleostei, Ostariophysi, Cypriniformes;
ZFIN; ZDB-GENE-980526-68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007407; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; P53_like_DNA_bnd.
InterPro; IPR00980; SH2.
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:transcription factor activity; IEA.
GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000960; P53_like_DNA_bnd.
InterPro; IPR001217; STAT.
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EMBL; AJ005693; CAA06677.1; -.
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                  86.8%; Score 694.5; DB 2;
86.4%; Pred. No. 2e-51;
live 10; Mismatches 10;
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86.4%; Pred. No. 2e-51;
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Pfam; PP01017; STAT alpha; 1.
Pfam; PP02864; STAT_bind; 1.
Pfam; PP02865; STAT_int; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                    Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
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Matches 133; Conservative
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NCBL_TaxID=7955;
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PROSITE; PS50001;
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765 AA;
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                                                                                                                           NCBI_TaxID=8090;
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Q6GUE7
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                                          1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
Gaps
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; FS3_like_DNA_bnd.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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85.7%; Pred. No. 3.4e-51;
iive 12; Mismatches 9; Indels 1.
  10; Mismatches 10; Indels
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Johnson M.C., Mourich D.V., Leong J.C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U60333; AAB60926.1;
HSSP; P42227; 1BG1.
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Last annotation update)
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  Matches 133; Conservative
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25-OCT-2004
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Q6DVF3;
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Q6DVF3
ID Q6DVF
AC Q6DVF
DT 25-OC
DT 25-OC
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LGEIDQQYSRFLQENNVLYQHNLRRIKQHLQSKYLEKPMEIARIVARCLWEEQRLLQT-A 119
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Submitted (Mart-2004) to the EMBL/GenBank/DDBJ databases.

Bubitted (Mart-2004) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005634; C:nucleus; IEA.

GO; GO:0000717; F:signal transducer activity; IEA.

R GO; GO:00007242; P:intracellular signaling cascade; IEA.

R GO; GO:00007255; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR008967; P53_like_DNA_bnd.

R InterPro; IPR001217; STAT.

R Pfam; PF00117; STAT.

R Pfam; PF01017; STAT_alpha; 1.
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05-JUL-2004 (TrEMBLE). 27, Last annotation update)
Signal transducer and activator of transcription 3 isoform 1.
Oryzias latipes (Medaka fish) (Japanese ricefish)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neoperygii; Percomorpha, Acanthoperygii; Percomorpha; Acanthoperygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
Signal transducer and activation of transcription factor 3. Oryzias latipes (Medaka fish) (Japanese ricefish). Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii, Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AY639947, AAT64912.1; -. GO, GO:0005634; C:nucleus, IEA.
GO, GO:0006871; F:signal transducer activity, IEA.
GO, GO:0003700; F:transducer activity, IEA.
GO, GO:0007242; P:intracellular signaling cascade; IEA.
GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; P53_like_DNA_bnd.
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                                                                                                                                                                                                                                                                                                                                               Liu R., Hong Y., Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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Best Local Similarity 85.1%; Pred. No. 1.1e-50;
Matches 131; Conservative 11; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
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SOR REPORT OF THE PROPERTY OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                1 MAQWNQLQQLETRYLEQLYHLYSDSFPMELRQFLAPWIESQDWAYAANKESHATLVFHNL 60
                                                                                                                                                                                                                                                                                                                        1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
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GO; GO:0005634, C:nucleus, IEA.
GO; GO:0003700; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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                                                                                                                                                                                DB 2; Length 785;
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                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307106; AAL09415.1; -.
                                                                                                          81F231BDE27DE938 CRC64;
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87411 MW; E661FFE18BEFD8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                         85.7%; Score 685.5; DB 2
85.1%; Pred. No. 1.2e-50;
ive 11; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKR 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodon fluviatilis (Puffer fish)
                                                                                                          89643 MW;
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Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SMART; SM00252; SH2; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                             Best Local Similarity 55.1.
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 132; Conservative
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                                                                                                          785 AA;
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PROSITE;
SEQUENCE
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                                                                                                          SEQUENCE
                                                                                                                                                                                Query Match
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61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21098508; PubMed=11164887; DOI=10.1016/S0145-305X(00)00050-1; Turpen J.B., Carlson D.L., Huang C.; "Cloning and developmental expression of Xenopus Statl."; Dev. Comp. Immunol. 25:219-229(2001).
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR0008967; P53 like_DNA_bnd.
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                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 50.1%; Score 401; DB 2; Length 751; Best Local Similarity 48.7%; Pred. No. 4e-26; Matches 75; Conservative 33; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Turpen J.B., Carlson D.L., Huang C.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY101602; AAM51552.1; -.
HSSP; P42224; 1BF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86497 MW; 788810A08B0889EA CRC64;
                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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751 AA
                                                                                                                                                                         Xenopus laevis (African clawed frog)
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Pfam; PF01017; STAT_alpha; 1.
Pfam; PF0264; STAT_bind; 1.
SMART; SM00252; SH2; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001217; STAT.
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                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
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PROSITE; PS50001
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Search completed: May 5, 2005, 14:57:40 Job time : 43.6706 secs THIS PAGE BLANK (USPTO)

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Sequence 12, Appl
Sequence 12, Appl
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 780, App
Sequence 780, Appl
Sequence 329, Appli
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                                                                                                                                                                          5, 2005, 14:59:00 ; Search time 114.139 Seconds (without alignments) 792.064 Million cell updates/sec
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1 RCLWEESRLLQTAATAAQQG.....LNYQLKIKVCIDKDSGDVAA 271
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1: \cgn2 \( \) \cgn \( \) 
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-876-773-12
US-10-380-020-4
US-10-380-020-2
US-10-380-020-5
US-10-045-792-8
US-10-045-792-8
US-10-0117-087-2
US-09-925-302-780
US-09-925-302-780
US-09-925-302-780
US-09-116-275-329
US-10-116-275-329
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq
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No.
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Sequence 14, Appl Sequence 15, Appl Sequence 21, Appl Sequence 30, Appl Sequence 31, Appl Sequence 22, Appl Sequence 22, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 20, Appl Sequence 2, Appl Sequence 3, Appl Sequence 4, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl Sequence 35, Appl Sequence 56, Appl Seque	س ن
US-10-090-185-14 US-10-090-185-18 US-10-090-185-18 US-10-090-185-18 US-10-090-185-30 US-10-090-185-30 US-10-090-185-30 US-10-090-185-29 US-10-090-185-29 US-10-090-185-29 US-10-090-185-29 US-10-090-185-29 US-10-090-185-19 US-10-090-185-12 US-10-090-185-12 US-09-873-205-4 US-10-090-185-12 US-09-876-773-4 US-09-876-773-4 US-09-876-773-4 US-09-876-773-4 US-09-876-773-4 US-09-876-773-4 US-09-876-773-4 US-10-245-120-1 US-10-245-120-1 US-10-245-120-1 US-10-245-120-1 US-10-245-120-1 US-10-245-120-1	US-09-833-205-6 US-09-876-773-8
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## ALIGNMENTS

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Sequence 9, Application US/10090185

Sequence 9, Application US/10090185

Sequence 9, Application No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui

APPLICANT: Horvath, Curt M

APPLICANT: Darrial Jar., James E

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: UNDER: 2002-03-04

PRIOR APPLICATION NUMBER: 09/387,418

PRIOR PRING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin On One of the original of the or
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100.0%; Score 1388; DB 13; Length 271;

Best Local Similarity 100.0%; Pred. No. 2.7e-110;

Matches 271; Conservative 0; Mismatches 0; Indels 0;
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NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                  121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                                                                                                                     227 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 286
                                                                                                                                                                                                                                                                                                         287 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
                                                 107 RCLWEESKLLOTAATAAQQGGGANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKWKVVE
                                                                                                                                                                                                                                                                                    181 LOOKVSYKGDPIVOHRPMLEERIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVQFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-MOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                        347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Darnell Jr., James E. Schindler, Christian W. Fu, Xian-Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-639-617-12; Sequence 12, Application US/10639617; Publication No. US20050079543A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FELEPHONE: 201 487-5800
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TELEX: 133521
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SEQUENCE CHARACTERISTICS:
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STATE: New Jersey
COUNTRY: USA
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AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                         LOOKVSYKGDPIVOHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhong, Zhong
TITLE OF INVENTION: RECREPTOR RECOGNITION FACTORS, PROFEIN SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
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le-109;
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             241 TKVRLLVKFPELNYOLKIKVCIDKDSGDVAA 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12
                                                                                                                                                                                 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     KESOU.

US-09-876-773-12

; Sequence 12, Application US/09876773

; Publication No. US20040058318A1

; GENERAL INFORMATION:

; APPLICANT: Darnell Jr., James E.

; Schindler, Christian W.

Fu, Xian-Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12
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Zhong, Zhong
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCES: 25
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COUNTRY: USA
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APPLICANT: YU, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REPRENCE: 18073-009-999
CURRENT APPLICATION NUMBER: 40/210/380,020
CURRENT PILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
LENGTH: 769
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APPLICANT: Yu, Hua.
APPLICANT: Pardoll, Drew
APPLICANT: Pardoll, Drew
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 5.
LENGTH: 769
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Pred. No. 9.1e-109;
1; Mismatches 1;
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                          241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA
                                                                                                                                                                               Sequence 2, Application US/10380020; Publication No. US20040052762A1; GENERAL INFORMATION:
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; Publication No. US20040052762A1
; GENERAL INFORMATION:
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Best Local Similarity 99.3
Matches 269; Conservative
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Publication No. US20040052762A1

GENERAL INFORMATION:

APPLICANT: Vu, Hua

APPLICANT: Datton, William

TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof

FILE REFERENCE: 10873-009-999

CURRENT APPLICATION NUMBER: US/10/380,020

CURRENT FILING DATE: 2003-03-07

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.0

SEQ ID NO 4
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                                                                                                                                  100.0%; Score 1388; DB 17;
100.0%; Pred. No. 1e-109;
iive 0; Mismatches 0;
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                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
TYPE: amino acid
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Best Local Similarity 100.
Matches 271; Conservative
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ORGANISM: Homo Sapiens
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APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REPRENCE: 184767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR PILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 56
LENGTH: 770
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                                                                                                                Score 1377; DB 14;
Pred. No. 9.1e-109;
1; Mismatches 1;
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OTHER INFORMATION:
            MOLECULE TYPE: protein
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-045-792-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 56, Application US/10038010; Publication No. US20030040089A1; GENERAL INFORMATION:
                                                                                                                    Query Match
Best Local Similarity 99.3%;
Matches 269; Conservative
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ORGANISM: Homo sapiens
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US-10-038-010-56
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                                                                                     Length
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                Score 1377; DB 15;
Pred. No. 9.1e-109;
1; Mismatches 1;
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Eq., David A.
REGISTRATION NUMBER: 26, 742
REFERENCE/DOCKET NUMBER: 600-1-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/045,792
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APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: <Unknown>
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10045792; Publication No. US20030003563A1. GENERAL INFORMATION: APPLICANT: Vinkemeier, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELEPHONE: 201-487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
                                                                                Query Match
Best Local Similarity 99.3
Matches 269; Conservative
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TYPE: PRT
ORGANISM: Homo Sapiens
US-10-380-020-5
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US-10-045-792-8
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190 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 249
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                                                                 Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.

TITLE OF INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: NUCleic Acids, Proteins and Antibodies

FILE REFERBNCE: PA104

CURRENT FILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SEQ ID NO 780

LENGTH: 793
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Pred. No. 9.4e-109;
1; Mismatches 1;
                                                             Query Match
99.2%; Score 1377; DB 9;
Best Local Similarity 99.3%; Pred. No. 9.4e-109;
Matches 269; Conservative 1; Mismatches 1;
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Best Local Similarity 99.3
Matches 269; Conservative
    ; ORGANISM: Homo sapiens
US-09-925-302-780
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US-09-925-302-780
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107 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE 166
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; Sequence 780, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: ROSen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR PILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver: 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
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                                                                                                                                                                                         Sequence 2, Application US/10117087
; Sequence 2, Application US/20030166854A1
; GENERAL INFORMATION:
; APPLICANT: SERUDI-CRESCENII, Ottaviano
; APPLICANT: DELLA PIETRA, Linda
; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
; FILE REFERENCE: SERLUPI=2;
; CURRENT APPLICATION NUMBER: US/10/117,087
; CURRENT FILING DATE: 2002-04-08
; PRIOR FILING DATE: 2000-03-19
; NUMBER OF SEQ ID NOS: 19
; SOFFWARE: Patentin version 3.0
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Pred. No. 9.1e-109;
1; Mismatches 1;
                                                                               347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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Best Local Similarity
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ORGANISM: Human
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LENGTH: 770
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Sequence 14, Application US/10090185

Sequence 14, Application US/20020197647A1

Sequence 14, Application No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Analy, Xiaokui

APPLICANT: Horvath, Curt M

APPLICANT: APPLICANT: NUMBER E

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: UNMBER: US/10/090,185

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14

LENGTH: 252
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                                                                                                               1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
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                                 Length 770;
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                                 Score 1372; DB 15;
Pred. No. 2.4e-108;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                   Query Match
Best Local Similarity 98.9%;
Matches 268; Conservative
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CRGANISM: Mus musculus
US-10-090-185-14
JS-10-116-275-349
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Sequence 329, Application US/10116275

Sequence 329, Application No. US20030211476A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Hagins, Lisa
APPLICANT: Hagins, Lisa
APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
CHURENT: Higgins, Lisa
APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
CHURENT: Higgins, Lisa
APPLICANT: WOMBER: US/10/116,275
CURRENT APPLICATION WUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOSTWARE: PATENTING PATE: 2002-10-04
NUMBER OF SEQ ID NOS: 331
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SEQ ID NO 349
LENGTH: 770
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Best Local Similarity 98.9%;
Matches 268; Conservative
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ORGANISM: Homo sapiens
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US-10-116-275-349
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US-10-116-275-329
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LENGTH: 770
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RESULT 15

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US-10-090-185-15

Squence 15, Application US/10090185

Publication No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Waresaczynska, Melissa H

APPLICANT: Horvath, Curt M

APPLICANT: Darnell JT., James E

TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR FILE REPRENCE: 600-1-253

FILE REPRENCE: 600-1-253

CURRENT APPLICATION NUMBER: US/10/090,185

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VOT: 2.0

SEQ ID NO 15

LENGTH: 236
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ORGANISM: Mus musculus
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(c) 1993 - 2005 Compugen Ltd.
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US-08-917025-12
US-08-212-185-12
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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Cutr M
APPLICANT: Horvath, Cutr M
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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US-09-387-418A-31
US-09-387-418A-30
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; Sequence 12, Application US/08369796
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APPLICANT: Zhong Zhong
TITLE OF INVENTION: FRUCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS.:
CORRESPONDENCE ADDRESS.:
STATEST: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RCLWEESRILLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 770;
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100.0%; Score 1388; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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; Sequence 12, Application US/08820754
; Patent No. 5976835
GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W., APPLICANT: Fu, Xian-Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                               New Jersey
: USA
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                                                                                                                                                            Hackensack
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                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                 STATE:
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    GENERAL INFORMATION:

APPLICANT: James E. Darnell, Jr.

APPLICANT: Zilong Wen

APPLICANT: Zilong Wen

APPLICANT: Curt M. Horvath

APPLICANT: Zilong Wen

APPLICANT: Zilong Zilong Wen

TITLE OF INVENTION: PUNCTIONALLY ACTIVE REGIONS OF SIGNAL

TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOOKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
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                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1388; DB 1;
100.0%; Pred. No. 1.7e-118;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: JACKSON ESQ., DAVId A.
REGISTRATION NUMBER: 26,742
REFERENCE/POCKET NUMBER: 600-1-116
TELEPHONE: 201 487-580
TELEPAX: 201 343-1684
TELEPX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Patent No. 5883228
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr. APPLICANT: Zijong Wen
                                                                                                                                                                                                                             STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
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; MOLECULE TYPE: protein
US-08-369-796-12
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-852-091-12
                                                                                                                                                                                                                                                                                                 COUNTRY:
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Best Local S
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347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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APPLICATION NUMBER: US/08/956,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                            US-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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Best Local Similarity 100.0
Matches 271; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKNQQLEQMLTALDQMRRSIVSELAGLLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 770;
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
CORRESPONDENCE ADDRESS: 25
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: ALauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STREET: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 13-MOV-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: US 09/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1388; DB 2;
100.0%; Pred. No. 1.7e-118;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDTUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
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TELEPHONE: 201 487-5800
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
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APPLICANT: Darnell Jr., James B.

APPLICANT: Schindler, Christian W.

APPLICANT: Fu, Xian-Yuan

APPLICANT: Fu, Xian-Yuan

APPLICANT: Zhong, Zhong

TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber F. T.

STRRET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-WAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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121 AMEYVQKTLITDEBLADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
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                                                                                                                                                                                                                                                                                                                                                                           61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                107 RCLWEESRLLOTAATAAQQGGQANHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVE 166
                                               1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
0; Gaps
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APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Fu, Xian-Yuan
APPLICANT: Schindler, Schindler, Schindler, Title OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES. 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
Indels
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  0; Mismatches
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 343-1684
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 12-MAR-1993
FILING DATE: 24-SER-1993
ATTORNEY AMBRICATION:
AMBRICATION NUMBER: US 08/126,588
FILING DATE: 24-SER-1993
ATTORNEY AMBRICATION:
AMBRICATION NUMBER: US 08/126,588
FILING DATE: 24-SER-1993
ATTORNEY AMBRICATION:
AMBRICATION NUMBER: US 08/126,588
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APPLICATION NUMBER: US/08/948,547
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271; Conservative
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MEDIUM TYPE: Floppy
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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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                                                            227 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 286
                                                                                                                                240
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                                                                                                                             LOOKVSYKGDPIVOHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT
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APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Abong, Zhong
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Harber
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/956,869
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                             347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: JGCKSON ESG., DAVIG A
RECISTRATION NUMBER: 26,742
RESISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 C
TELECHORE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L. A L. L. A L. L. L. A L. L. L. L. L. L. Klauber & Jackson LIRET: 411 Hackensack Avenue CITY: Hackensack Avenue STATE: New Jersey COUNTRY: USA ZIP: 07601
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APPLICATION NUMBER: 08/212,185
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08956869 Patent No. 6030808
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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amino acid
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Best Local Similarity
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US-08-956-869-12
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-956-653A-12
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                                                                                                                                                                                                                                                                                                               NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                                                                                                                                                                                                                        AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                                                                                                                                                                                                                                                                                       LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE 166
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Patent No. 6235873
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
FILLE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 199-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTING WORLS: 2.0
SEQ ID NO 3
LENGTH: 770
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                                                                                                                                                                        100.0%; Score 1388; DB 3; Length 770; 100.0%; Pred. No. 1.7e-118; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                LENGTH: 770 amino acids

17YPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-948-547-12
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 770 amin-
                                                                                                                                                                      Query Match 100.9
Best Local Similarity 100.
Matches 271; Conservative
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; ORGANISM: Mus musculus
US-09-364-970-3
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US-09-364-970-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                               APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AMEYVQKTLIDBELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Darrell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; DB 3;
1.7e-118;
347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;; Score 1388; D
;; Pred. No. 1.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 12, Application US/08956653A; Patent No. 6338949; GENERAL INFORMATION:
                                                                                                                                   Sequence <5, Application US/09364970; Patent No. 6235873; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.(
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Mus musculus
US-09-364-970-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Jersey
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STATE: New Jerse
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121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 NIQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 770;
    FITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
ALTING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson ESQ., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1388; DB 4; Best Local Similarity 100.0%; Pred. No. 1.7e-118; Matches 271; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600-1-073 CIP
                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAVE: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                   E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 770 amino acids amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                               Hackensack
: New Jersey
RY: USA
                                                                                                                                                                                ZIP: 07601
                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
PCT-US95-17025-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347
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Patent No. 6605442

GENERAL INFORMATION:
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                       SOFTWARE: Patentin 1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1388; DB 3; 100.0%; Pred. No. 1.7e-118;
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                                                                                                        FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-WAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-195
IBM PC compatible
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TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LELEFAX: 201 343-5800
LELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amin
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amino acid
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Best Local Similarity
Matches 271; Conserva
                         OPERATING SYSTEM:
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US-08-212-185-12
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Gaps .. 9

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61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 AMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
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Pred. No. 1.7e-117;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-65825/1994
FILING DATE: 04-APR-1994
ATTORNEY/AGBNT INFORMATION:
NAME: Nakamura, Dean H.
                                                                                                                                                               3: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 Pennsylvania Avenue, N.W.
                                                                                           TRANSCRIPTION FACTOR APRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moarefi, Ismail
Darnell, Jr., James E.
    Patent No. 5719042
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTIYON: TRANSCRIPTIC
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 8, Application US/09012710; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe APPLICANT: Moarefi, Ismail; APPLICANT: Darnell, Jr., James E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,981
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.3
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                              20037
                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-416-581B-9
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                                 APPLICANT: James E. Darnell, Jr.
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Zilong Zhong
Zhong Zhong Zhong Zhong
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
AUGHBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREE: 411 Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 226
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CARRENT APPLICATION DATA:
APPLICATION NAMBER: PCT/US95/17025
FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1388; DB 5;
100.0%; Pred. No. 1.7e-118;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201,487-5800
Sequence 12, Application PC/TUS9517025
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-416-581B-9
; Sequence 9, Application US/08416581B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 343-1684
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                          New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION;
                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
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                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLODDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
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Kuriyan, John
VENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A VENTION: STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                       ZIP: 07601

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1377; DB 3;
Pred. No. 1.7e-117;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
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                                                                                            ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,72
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09556273; Patent No. 6312887; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             201-487-580C
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
STRANDEDNESS: sir.'
TOPOLCGY: '
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NO
                                                                            CORRESPONDENCE ADDRESS: ADDRESSE: Klauber &
                                                         NUMBER OF SEQUENCES:
                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                       New Jersey
: USA
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Best Local Similarity
                                                                                                                            CITY: Hackensack
STATE: New Jerse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                     COUNTRY:
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US-09-556-273-8
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227 AMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT
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IITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
99.2%; Score 1377; DB 3;
Best Local Similarity 99.3%; Pred. No. 1.7e-117;
Matches 269; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                               411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5, 2005, 14:58:52
                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REPERENCE/DOCKET NUMBER: 600-1 TELECHMUNICATION INFORMATION: TELEPHONE: 201-487-5800 TELEFAX: 201-343-1684
                       NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                 New Jersey
: USA
                                                                                             STREET: 411 Hack
CITY: Hackensack
STATE: New Jerse
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                                                                                                                                                                COUNTRY: US/
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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226

APPLICANT: Vinkemeier, Uwe
APPLICANT: Warefi, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Wariyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A

us-10-090-185-9.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May Run on:

5, 2005, 14:55:35 ; Search time 84.1694 Seconds (without alignments) 1245.251 Million cell updates/sec

Title: Perfect score:

US-10-090-185-9 1388 1 RCLWEESRLLQTAATAAQQG.......INYQLKIKVCIDKDSGDVAA 271

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_16Dec04:\* 1: genesecm1000r: .. Database

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aay72841 Mouse Sta	Aar72082 Mouse Sta	Aaw03176 Mouse STA	Aae22055 Human Sta	Abb57164 Mouse isc	Aae22054 Human Sta	Aae22056 Human pro	Aar82995 Mouse liv	Aay03768 Human STA	Aab12377 N-termina	Aae14652 Murine ST	Abg69497 Human bai	Abul0476 Mouse STA	Adn04365 Antipsori	Adp54789 Human PRO	Aab58442 Lung canc	Add44738 Rat Prote	Human	Aab19964 Human sig	Human	Add44740 Human Pro	Aay72846 Mouse Sta	Aay72847 Mouse Sta	Aay72850 Mouse Sta	Aay72863 Mouse Sta
QI	AAY72841	AAR72082	AAW03176	AAE22055	ABB57164	AAE22054	AAE22056	AAR82995	AAY03768	AAB12377	AAE14652	ABG69497	ABU10476	ADN04365	ADP54789	AAB58442	ADD44738	AAR82993	AAB19964	AAE15174	ADD44740	AAY72846	AAY72847	AAY72850	AAY72863
DB	4	N	7	Ŋ	Ŋ	Ŋ	Ŋ	~	7	'n	S	ហ	9	ω	œ	٣	7	~	4	Ŋ	7	4	4	4	4
% Query Match Length	271	770	770	720	769	169	169	770	770	770	770	770	770	770	770	793	770	770	770	770	770	252	236	229	229
% Query Match	100.0	100.0	100.0	99.2	99.5	99.2	99.2	99.2	99.2	99.2	99.2	99.2	99.2	99.2	99.2	99.2	0.66	98.8	98.8	98.8	98.8	92.9	87.3	84.4	84.1
Score	1388	1388	1388	1377	1377	1377	1377	1377	1377	1377	1377	1377	1377	1377	1377	1377	1374	1372	1372	1372	1372	1290	1212	1172	1168
Result No.	п	7	٣	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

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Mous Mous Mous Mous Mous Mous Mous Huma Huma Huma	Human Human
Aay72862 Aay72861 Aay72854 Aay72854 Aay72858 Aay72858 Aay72849 Aay72849 Aay72844 Aay72844 Aay72844 Aay72844 Aay72844 Aay72844 Aay72844 Aay72844 Aay72844 Aay72844 Abright Aay720495 Aay72049	Abu04745 Abu04743
AAY72862 AAY72861 AAY72860 AAY72854 AAY72855 AAY72855 AAY72856 AAY72856 AAY72856 AAY72856 AAY72856 AAY72850 AAY72850 AAY72850 AAY72850 AAY72850 AAY72850 AAY72850 AAY72850 AAY72850 AAY72850 AAY72850	ABU04745 ABU04743
4 4 4 4 4 4 4 4 4 4 5 6 6 6 6 6 6 6 6 6	99
222 2222 2222 2222 2222 2222 2222 2222 2222	712
4 8 8 8 8 6 6 6 7 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	46.6 46.6
111 112 111 101 111 111 111 111 111 111	647 647
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44 45

## ALIGNMENTS

```
Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                     Mouse Stat3 protein fragment #2 (107-377 amino acids).
                                                                                 Location/Qualifiers
     AAY72841 standard; protein; 271 AA.
                           (first entry)
                                                                       Mus musculus.
                           31-MAY-2001
                AAY72841;
                                                             therapy.
                                                                                  Key
Region
AAY72841
```

24. .48 /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein" /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein" 30-AUG-2000; 2000WO-US023822. 236. .252 WO200116605-A2. 08-MAR-2001 Region

99US-00387418. 31-AUG-1999;

(UYRQ ) UNIV ROCKEFELLER.

Horvath C, Zhang X,

Darnell JE; Wrzeszcynska MH,

WPI; 2001-226705/23.

Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.

Claim 65; Page 67-68; 86pp; English.

The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the Cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a

Claim 1; Page 107-110; 160pp; English.

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120
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 transcription factor such as c-Jun and a Stat protein such as Stat-1 and
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           Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. Stat protein comprises the N-terminal domain, coiled-coil domain, bNA binding domain, linker domain, SH2 domain and transactivation domain.
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                                                                                                                        100.0%; Score 1388; DB 4; 100.0%; Pred. No. 2.7e-116;
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(first entry)
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Best Local Similarity
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27-SEP-1995
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genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.

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                         A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 KDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339 +40) were cloned in plasmids 13sfl and 19sf6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-2003 to correct PN field.)
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disease; antagonist; therapy.
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                                                                                                                                                                                                          Length 770;
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                                                                                                             STATA (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STATA can be obtd. using cDNA clone 198f6 (AAT31278) obtd. from splenic/thymic cells. STATA includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery via DNA binding in a receptor-ligand specific manner. STAT proteins and their DNA binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and
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                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                     Mouse signal transducer and activator of transcription (STAT)
                                                                                                                                                                                                                                                                                    Length 770;
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                                                                           Disclosure; Page 87-90; 138pp; English
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Best Local Similarity
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The invention trainers to a mention of modutating anglements and interior response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription of 3 (Statal). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, toronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, tranma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, cyprential angiopathy chronic active hepatitis, corrective tissue disease, primary biliary cirrhosis, pernicious mixed connective tissue disease, primary biliary cirrhosis, pernicious connective tissue disease, primary biliary cirrhosis, pernicious disease, rheumancoid arthritis, disopathic Addison's disease, victiligo, cyprentially, autoinmune neutropenia myaathenia gravis, dispathic chrombocytopenia purpura, Grave's disease, condense, autoinmune chronic caretive collitis and chese deposit disease. The method is useful in preventing or treating appending appending a specific proliferative and oncogenic disease which includes sarcomas and propertions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
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Pred. No. 9.6e-115;
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/note= "Encoded by ACA CCA TTC"
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                                                                                                                                                                                                                                                                                      10-SEP-2001; 2001WO-US028254.
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N-PSDB; AAD35066.
Misc-difference 713
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UNIV SOUTH
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Best Local Similarity
Matches 269; Conserv
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226 180 286

167 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 226

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conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to AB19912, or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic condition related sequence, which are used in the exemplification of the present invention
                  LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
LQQKVSYKGDP1VQHRPMLEER1VELFRNLMKSAFVVERQPCMPMHPDRPLV1KTGVQFT
                                                                                                                                                                                                                                                                                                         Mouse ischaemic condition related protein sequence SEQ ID NO:398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for examining ischaemic
                                                                                                                                                                                                                                                                                                                                          Mouse, ischaemia, compressive ischaemia, occlusive ischaemia, vasospastic ischaemia, ischaemic condition, ischaemic disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagata T,
                                                                                           TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                       TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA
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181
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1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE

Matches 269; Conservative

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Similarity

Local

Gaps

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61 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120

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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
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                                                                                                                    346
  180
                                      286
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                        227 AMEYVOKTLIDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
                                                                                                  287 LQQKVSYKGDPIVQHRPMLBERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT
  121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
                                                                             LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; anglogenesis; myocardial infarction; hypoplycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory disress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; drave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
                                                                                                                                                           271
                                                                                                                                                                                  347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                   Human Stat3 protein.
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nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, Siogran's syndrome, sclerodarma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary billary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's idiopathic thrombocytopenia purpura, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, ilposarcoma, degenerative discorders, growth deficiency, hypoproliferative disorders, phydical treauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3
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Sequence 769 AA;

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AMEYVOKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                                                                                                                                             AMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 286
                                                                                                                                                                                                                                                                                                                 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
                                                                                                                                                                                                                                                                                                                                      LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
                                                                                                                   107 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE 166
                                                                                                                                                         NLODDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
                                                                                                                                                                                                NLODDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 226
                                                                              RCLWEESRILLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
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99.2%; Score 1377; DB 5; Length 769; 99.3%; Pred. No. 1e-114; Live 1; Mismatches 1; Indels (
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les 269; Conserv
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AAE22056 standard; protein; 769 AA (first entry) 25-JUL-2002 AAE22056; RESULT

Human; signal transducer and activator of transcription 3; ischaemia; Human protein related to angiogenesis regulation.

immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypozylycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.

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346

TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271

287 241

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Homo sapiens

WO200220032-A1

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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing thypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, introgen necrosis, proliferative andiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating asymptom of an autoimmune disease such as systemic lupus carthematosus, multiple sclerosis, insulin dependent diabetes mellitus, sjogren's syndrome, sclerosis, insulin dependent diabetes mellitus, sjogren's syndrome, sclerosis, insulin dependent diabetes mellitus, sjogren's syndrome, sclerosis, polymyositis, chronic active hepatitis, and anacemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, connective tissue disease, primary bilary cirrhosis, penthicinus careinous and energy bilary vulgaris, autoimmune thyroiditis, idiopathic Addison's disease, intenting a disease, connective disease the method is useful in preventing or treating especific proliferative and oncogenic disease which includes sarcomes and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, libroarcoma, liboarcoma, degenerative disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, hypoproliferative disease repubation related to angiogenesis regulation
                                                                                                                                                                                                                                                                                  Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
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1; Mismatches
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                                                                                08-SEP-2000; 2000US-0231212P
                                           10-SEP-2001; 2001WO-US028254
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                                                                                                                            (UYSF-) UNIV JOHNS HOPKINS (UYSF-) UNIV SOUTH FLORIDA
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The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. ARFF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
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Pred. No. 1e-114;
1; Mismatches 1;
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TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                     Mouse liver acute phase response factor.
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                                                                                                                                                         AAR82995 standard; protein; 770 AA
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                                                                                                                                                                                                                         AAR82995;
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The present sequence represents a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. The encoding sequence differs from the original published human STAT3 gene sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3 DTA molecule can be used for the recombinant expression of the variant. STAT3 protein is useful as a medicament or pharmaceutical composition for treatment of autoimmune or inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIQDDFDFNYKTLKSQCDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
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                                                                                                                                                                                                 Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKWKVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human Signal Transducer and Activator of Transcription 3 (STAT3) allelic variant useful for treatment of autoimmune and inflammatory
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347 TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                         (ISTF ) ARS APPLIED RES SYSTEMS HOLDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Della Pietra
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                                                                                                                                                                                                                                                                                                                                                                               97EP-00116061
                                                                                      AAY03768 standard; protein;
                                                                                                                                                                          Human STAT3 allelic variant
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Best Local Similarity 99.3
Matches 269; Conservative
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                                                                                                                                              11-JUN-1999
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Length 770; 1; Indels 166

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The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than 5.0 Angerome. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.
                                                                                                                                                             , signal transducer and activator of transcription; crystal; design; murine.
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                                                                                                                                                                                                                                                                                         alpha helix
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N-terminal domain of murine STAT-3 protein.
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                                                                                                                                                                                                                                                                                         3(10) helix of
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/label= Alpha helix 1
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|abel= Alpha helix 2
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/label= Alpha helix 3
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/label= Alpha helix 7
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/label= Alpha helix 5
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/label= Alpha helix 8
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                                                                     AAB12377 standard; peptide; 770
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/label= Alpha
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/label= Alpha
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leukaemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that binds to the N-terminal domain of a STAT protein, identifying a compound that enhances or diminishes the binding of the dimeric STAT proteins to each other and/or their nucleic acid binding site, or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under
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    /note= "Conserved N-terminal domain of the STAT family"

                                                                                                                                                                                                                                                      107 RCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
                                                                                                                               167 NLODDFDFNYKTLKSGGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
                                                                                                                                                                           AMEYVOKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESOLQTRQQIKKLEE
                                                                                                                                                                                            227 AMEYVQXTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE
                                                                                                                                                                                                                                      LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT
                                                  RCL/WEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE
                                                                                                             NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying compounds that bind to signal transducer and activator of transcription proteins, useful for the production of new drugs.
                   Gaps
                    ;
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal transducer and activator of transcription; STAT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuriyan J;
    Pred. No. 1e-114;
                                                                                                                                                                                                                                                                                                                     TKVRLLVKFPELNYOLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                   TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viral disease; growth retardation; murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              AAE14652 standard; protein; 770 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Col 47-50; 44pp; English
                    1;
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   99.3%;
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                    Conservative
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Best Local Similarity
Matches 269; Conserv
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Query Match

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the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new drugs. An antagonist of STAT N-terminal dimeric interactions that inhibits the binding of the STAT dimers to adjacent weak binding sites on a promoter of a gene, could be useful as drugs in the treatment of diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other hand, an agonist of N-terminal dimeric interactions between STAT dimers, can be used as drugs in the treatment of diseases e.g. anaemia, neutropaemia, thrombocytopaemia, cancer, obesity, viral diseases and growth retardation. The present sequence is murine STAT3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286
                                                                                                                                                                                                                                                                                                                                     RCLWEESRLLQTAATAAQGGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                            AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, yeast two-hybrid assay, adipocyte, bait protein, NIDDM,
non-insulin diabetes mellitus, obesity, selected interacting domain, SID,
protein-protein interaction map, PIM, anorectic, metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders.
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(CNRS ) CENT NAT RECH SCI.
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Best Local Similarity 99.3
Matches 269; Conservative
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                                                                                                                                                                                               Sequence 770 AA;
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The invention relates to a complex of protein-protein interactions defined in the specification, or polynucleotides in adipocyte cells as defined in the specification, or polynucleotides in adipocyte cells as for the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the capression of which is toxic for the recombinant host cell which is transformed with two vectors, where the first vector comprises a polynucleotide encoding a first hybrid polypeptide and DNA binding domain the second vector comprising a polynucleotide encoding a second hybrid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and reporter gene, when the first and second hybrid polypeptides interact and recombinant host cell (i.e. using the yeast two-hybrid system). The complexes are useful for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic compound isolated by the method is useful for treating and preventing compound isolated by the method is useful for treating obesity or metabolic described the protein obesity or metabolic described and the proteins of the decompound isolated by the method is useful for treating obesity or metabolic described and preventing of the method is the decompound that the decompound isolated by the method is useful for treating obesity or metabolic decompound the decompound that the decompound the decompound that the d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the complex further define a set of selected interacting domains, SID. The present sequence represents a member of the protein complex of the invention, used as the bait protein in the yeast two-hybrid assay
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drug screening; STAT-STAT dimer interaction; STAT3.
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/label= alpha_helix_1
12. .21
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                            Claim 1; Page 54; 125pp; English.
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les 269; Conservative
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The invention relates to a crystal of an N-terminal domain of signal transducer and activator of transcription (STAT) protein, where the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the N-terminal domain of the STAT protein to a resolution of greater than 5.0 Angstrom. The methods and compositions are useful for the design and screening of drugs that enhance or inhibit STAT-STAT dimer interactions. The present sequence represents the amino acid sequence of mouse STAT3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLODDFDFNYKTLKSOGDMODLNGNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEE 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New crystal having an N-terminal domain of a STAT protein performing X-ray crystallographic studies, useful for screening drugs that enhance or inhibit STAT-STAT dimer interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLQDDFDFNYKTLKSQCDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
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                                                                                                                               contribute
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Pred. No. 1e-114;
; Mismatches 1; Indels
                                                                                                                               71
                                                                                                                                                                                94
              note= "Residues 19-21 form a 3 helix"
                                                                                                                               and
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                                                                                                                                                                                                                                                                                                                                                                                                                                Kuriyan J;
                                                                                                                               68
                                                                                                                                                                                90
                                                                                                                                                                                83, 86,
                                                                                                                                                                                       packing of the coiled-coil"
                                                                                                             /label= alpha_helix_6
/note= "Residues 57, 61, 64
packing of the coiled-coil"
77. .96
                                                                                                                                                                                                                                                                                                                                                                                                                               Darnell JE,
                                                 35. .40 _ _ _ _ /
/label= alpha_helix_4
                                                                         3. 47
label= alpha_helix_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 25-26; 46pp; English
                                                                                                                                                                                                       99. .119
/label= alpha_helix_8
                                     alpha_helix_3
                                                                                                                                                                 /label= alpha helix 7
/note= "Residues 79,
 'label= alpha helix
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24-APR-2000; 2000US-00556273.
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The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                     Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS
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TKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271
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pharmaceutical composition for diagnosing
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                                                                                                                                                 Antipsoriatic protein sequence #377.
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                                                                              ADN04365 standard; protein; 770
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Sequence 770 AA;

human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiantiastic; antiinflammatory; antipsoriatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; Human PRO protein sequence SEQ ID NO:765. ADP54789 standard; protein; 770 AA 28-OCT-2003; 2003WO-US034381. 29-OCT-2002; 2002US-0422472P (first entry) virucide; gene therapy 3, Clark H, Wu TD; (GETH ) GENENTECH INC WPI; 2004-376182/35 N-PSDB; ADP54788. WO2004039956-A2 Homo sapiens 13-MAY-2004. Aggarwal S, ADP54789; Wood WI, RESULT 15 ADP54789 

New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response

Gurney AL, Schoenfeld J, Williams PM;

Claim 1; SEQ ID NO 765; 3009pp; English.

The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptide; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4); (7) a composition of matter of the polypeptide or an antibody that binds to the polypeptide or an antibody that binds to the polypeptide or an antibody that binds to the manual; (10) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide in a sample suspected of having the polypeptide; (11) a method of disease or an inflammancery immune response in mammal; (12) a method of identifying a compound that inhibits or mincs the activity of or expression of a gene encoding a PRO polypeptide in mammal. The PRO sequences have antiallergic, antianaemic, antiarthritic, antiasthmatic, antialergic, antianaemic, antiarthritic, antidabetic, antiinflammatory, antipsoriatic, antithyroid, CNS, dermatological, gastrointestinal, haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular, nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid (I) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune response. The present sequence represents a human PRO protein from the present invention.

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181 LQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
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Aae14652 Aae15174 Abul0476 Add44738 Add44740 Adb54789 Adb54789 Adb54789 Aab54789 Aab54789 Aab54789 Aab72855 Aay72855 Aay72855 Aay72855 Aay72855 Aay72855

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## ALIGNMENTS

Breast ca Human PRO Protein e

Aab19965 Rae15175 Rabr47599 Rd182891 Rdp13003 Adr14069 Rdr14361 Adr14361 Rdr14361 Rdr14361

Human NF-Human NF-

Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein. Mouse Stat3 protein fragment #11 (155-249 amino acids). Darnell JE; Zhang X, Horvath C, Wrzeszcynska MH, AAY72853 standard; protein; 95 AA 31-AUG-1999; 99US-00387418. 30-AUG-2000; 2000WO-US023822 (first entry) (UYRQ ) UNIV ROCKEFELLER WPI; 2001-226705/23. WO200116605-A2 Mus musculus. 31-MAY-2001 08-MAR-2001. AAY72853; therapy. 

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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geneseqp2004s:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

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Database

SUMMARIES

Result No.

Mouse Human Mouse Description Aay72852 N
Aay72849 N
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The present sequence is mouse Stat3 protein fragment containing 155-249 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain

Claim 65; Page 78; 86pp; English.

Sequence 95 AA;

Human pla Human STA N-termina Human sig

Aay03768 B Aab12377 B Aab19964 B

AAR82995 AAR82993 AAY03768 AAB12377

AAB19964

Human Mouse us-10-090-185-21.rag

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Mouse Stat3 protein fragment #7 (107-249 amino acids)
                                 AAY72849 standard; protein; 143 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is mouse Stat3 protein fragment containing 155-282
                                                                                                                                                                                                                                                         Mouse, Stat3 protein, transcription factor, c-Jun; gene transcription, cellular transformation, dysproliferative disease, cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VQDLEQKMKVVENLQDDFDFDYKTLKSQGDMQDLNGNNQSYTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VQDLEQKMKVVENLQDDFPFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                             1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                        1 VQDLEQKWKVVENLQDDFDFDYKTLKSQGDWQDLNGNNQSVTRQKWQQLEQMLTALDQMR
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 128;
Score 477; DB 4; Length 95; Pred. No. 5.9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                       Indels
                                                                                                                                                                                                                                      Mouse Stat3 protein fragment #10 (155-282 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 477; DB 4;
100.0%; Pred. No. 8.3e-41;
ive 0; Mismatches 0;
                        ö
                                                                                         RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                     RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
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100.0%; Score 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 65; Page 78; 86pp; English.
                       0
                                                                                                                                                                    AAY72852 standard; protein; 128
            100.08;
                                                                                                                                                                                                                                                                                                                                                                       30-AUG-2000; 2000WO-US023822
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                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                        Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                           WO200116605-A2.
                                                                                                                                                                                                                                                                                                       Mus musculus.
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                       95;
                                                                                                                                                                                                                31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                  08-MAR-2001
                                                                                                                                                                                           AAY72852;
 Query Match
Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                     Matches
                                                                                                                                                          AAY72852
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49 VÓDLEQKAKVVENLÓDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKAQQLEQMLTALDQMR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is mouse Stat3 protein fragment containing 107-249 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                              /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VQDLEQKAKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 477; DB 4;
100.0%; Pred. No. 9.5e-41;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 65; Page 75-76; 86pp; English.
                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00387418.
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nes 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                        .48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 143 AA;
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ID AAY7
XX
AC AAY7
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therapy.

Key Region

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The present sequence is mouse Stat3 protein fragment containing 130-342 amino acids of Stat3 protein. This Stat3 fragment showed very weak binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a stranscription factor such as c-Jun and a Stat protein such as Stat-1 and Stat.3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                       1. .25
/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188. .204
/note= "Stat3-c-Jun interaction region 2; corresponds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 VQDLEQKMKVVENLQDDFDFNYKTLKSQCDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 213;
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100.0%; Pred. No. 1.5e-40;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Darnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wrzeszcynska MH,
                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-2000; 2000WO-US023822.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-226705/23.
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                                                                                                                                                                                                                                                                           WO200116605-A2
                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                             08-MAR-2001.
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                                                                                                                                          Region
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                                                                                                           Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is mouse Stat3 protein fragment containing 107-282 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
                                                                                                                                Mouse, Stat3 protein, transcription factor, c-Jun, gene transcription, cellular transformation, dysproliferative disease, cancer, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
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                                                                 Mouse Stat3 protein fragment #6 (107-282 amino acids).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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31-MAY-2001 (first entry)
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Best Local Similarity 100.
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200116605-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-1999;
                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-2001
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Zhang X,

AAY72851;

RESULT 5

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Gaps

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The present sequence is mouse Stat3 mutant protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Unn and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These indentifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 84

    .25
/note= "Stat3-c-Jun interaction region 1; corresponds to

             /note= "Wild type Lys substituted with Ala; corresponds to 348 position of Stat-3 protein"
                                                                                /note= "Wild type Arg substituted with Ala; corresponds to 350 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse Stat3 mutant (L148A,V151A,T346A,K348A,R350A) protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for use in modulating the interaction between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 477; DB 4;
100.0%; Pred. No. 1.6e-40;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying an agent for use in modulating the transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                              Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 66; Page 84-85; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY72860 standard; protein; 229 AA.
                                                                                                                                                                                                                                             30-AUG-2000; 2000WO-US023822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Quest Local Similarity 10v...
Best Local Similarity 10v...
Then 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                   (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                              Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 228 AA;
Misc-difference
                                                                Misc-difference
                                                                                                                                                        WO200116605-A2
                                                                                                                                                                                                                                                                                         31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                 08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY72860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Region
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/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is mouse Stat3 protein fragment containing 155-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of transformation diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKWQQLEQMLTALDQMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild type Thr substituted with Ala; corresponds to 346 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse, Stat3 protein, transcription factor, c-Jun; gene transcription, cellular transformation, dysproliferative disease, cancer, psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                          Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse Stat3 mutant (T346A, K348A, R350A) protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                    Darnell JE;
  342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 477; DB 4; Best Local Similarity 100.0%; Pred. No. 1.6e-40; Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 65; Page 79; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY72861 standard; protein; 228
                                                                                                                                                                               99US-00387418
                                                                                                                                   30-AUG-2000; 2000WO-US023822
                                                                                                                                                                                                                        (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; mutant; mutein.
                                                                                                                                                                                                                                                                    Horvath C,
                                                                                                                                                                                                                                                                                                              WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                              WO200116605-A2
                                                                                                                                                                               31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY72861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
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1. .25
Joute= "Stat13-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
213. .229
/note= "Stat13-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is mouse Stat3 protein fragment containing 130-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of transformation. These identifying agents are used in the treatment of Stat protein comprises and also for transing cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                      Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VQDLEQKWKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying an agent for use in modulating the interaction between transcription factor c\text{-Jun} and a Stat3 protein.
                                                                 Mouse Stat3 protein fragment #8 (130-358 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 477; DB 4; 100.0%; Pred. No. 1.6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 65; Page 76-77; 86pp; English.
                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-2000; 2000WO-US023822.
                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      WO200116605-A2
                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-1999;
                       31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2001
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                                                                                                                                                   therapy.
                                                                                                                                                                                                                                   Key
Region
                                                                                                                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY72863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130-358 amino acids of Stats procein. This mutant is obtained by replacing Leu 148 with Ala, Val 151 with Ala, Thr 346 with Ala, Ivs 348 with Ala and Arg 350 with Ala in the Stats] protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-un and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., restament of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation
                                                                                                          to
                                                                                                                                                                                                                                   t
                                                                                                                                                                                                                                                                                          /note= "Wild type Lys substituted with Ala corresponds to 348 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                         /note= "Wild type Arg substituted with Ala corresponds to 350 position of Stat-3 protein"
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                                         /note= "Wild type Leu substituted with Ala; corresponds to 148 position of Stat-3 protein"
                                                                                             /note= "Wild type Val substituted with Ala corresponds 151 position of Stat-3 protein"
                                                                                                                                                                                                                               Thr substituted with Ala corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is mouse Stat3 mutant protein fragment containing
                                                                                                                                             213. . . 229
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VODLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 VODLEOKMKVVENLODDFDFNYKTLKSOGDMODLNGNNOSVTROKMOOLEOMLTALDOMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 477; DB 4; Length 229; ; Pred. No. 1.6e-40; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Darnell JE;
130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95
                                                                                                                                                                                                              /note= "Wild type Thr substitut
346 position of Stat-3 protein"
Misc-difference 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY72850 standard; protein; 229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-2000; 2000WO-US023822
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Best Local Similarity 100..
Best Local Similarity 100..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Horvath C,
                                                                                                                                                                                                                                                                                                                                     Misc-difference 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-226705/23
                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 229 AA;
                                                                                                                                                                                                            Misc-difference
                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                        WO200116605-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY72850
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Gaps

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Length 229; Indels

domain

RESULT 9 AAY72850

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.25 /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"

location/Qualifiers

Misc-difference

Region

Region

Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;

therapy; mutant; mutein.

Mus musculus

Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids)

/note= "Wild type Leu substituted with Ala; corresponds to 148 position of Stat-3 protein" 223 229 "Stat3-d-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"

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/note= "Wild type Val substituted with Ala corresponds to
151 position of Stat-3 protein"
213. .229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is mouse Stat3 mutant (V151A) protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing Val 151 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                 Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; therapy; mutant; mutein.

    .25
/note= "Stat3-c-Jun interaction region 1; corresponds
130-154 position of Stat3 protein"

                                                                                                                                                                                                                                                                         /note= "Stat3-c-Jun interaction region 2; corresponds 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 477; DB 4;
Pred. No. 1.6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wrzeszcynska MH,
                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 66; Page 86; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2000; 2000WO-US023822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 229 AA;
                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                 WO200116605-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   31-AUG-1999;
                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                         Region
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Tdentifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.

Darnell JE;

Wrzeszcynska MH,

30-AUG-2000; 2000WO-US023822.

WO200116605-A2

08-MAR-2001

(UYRQ ) UNIV ROCKEFELLER Zhang X, Horvath C, WPI; 2001-226705/23.

31-AUG-1999;

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The present sequence is mouse Stat3 mutant (L148A) protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing Leu 148 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a star transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 477; DB 4; 100.0%; Pred. No. 1.6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 66; Page 85; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY72847 standard; protein; 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-2001
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
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Similarity

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31-MAY-2001 (first entry)

AAY72862;

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AAY72862

RESULT 11 AAY72862

RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI

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therapy

Key Region

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49 VQDLEQKWKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is mouse Stat3 protein fragment containing 107-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                              236. .252
/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
                                                                    /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 477; DB 4; Length 252; larity 100.0%; Pred. No. 1.8e-40; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Stat3 protein fragment #2 (107-377 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95
                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang X, Horvath C, Wrzeszcynska MH,
                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY72841 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 65; Page 73; 86pp; English
                                                                                                                                                                                                                                                                                                30-AUG-2000; 2000WO-US023822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       (UYRQ ) UNIV ROCKEFELLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 252 AA;
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                                                                                                                                                                                                                                                                                                                                             31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is mouse Stat3 protein fragment containing 107-342 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                     24. .48
/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
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                                            Mouse, Stat3 protein, transcription factor, c-Jun, gene transcription, cellular transformation, dysproliferative disease, cancer, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; Stat3 protein, transcription factor, c-Jun; gene transcription, cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mouse Stat3 protein fragment #5 (107-342 amino acids).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Darnell JE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wrzeszcynska MH,
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 65; Page 74; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 31-AUG-1999;
                                                                                                                                     Mus musculus.
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AAY72846;

RESULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 VQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 108
                                                                                                                                                                                                                                                                                                                              The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a method Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal transducer and activator of transcription; STAT; 19sf6; Stat3; receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VODLEQKWKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 60
/note= "Stat3-c-Jun interaction region 1; corresponds 130-154 position of Stat3 protein" 236. .252 /note= "Stat3-c-Jun interaction region 2; corresponds 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                    Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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Best Local Similarity 100.0%; Score 477; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 2e-40;
Matches 95; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                               Wrzeszcynska MH, Darnell JE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                                          Claim 65; Page 67-68; 86pp; English
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                                                                                                                                    30-AUG-2000; 2000WO-US023822
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                                                                                                                                                                                       (UYRQ ) UNIV ROCKEFELLER
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                                                                                                                                                                                                               Horvath C,
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A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89318) was isolated that encoded a 91 kDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89319-40) were cloned in plasmids 138fl and 198ff and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor recognition factor implicated in transcriptional stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VODLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                              93US-00126588.
93US-00126595.
94US-00212184.
94US-00212185.
94WO-US010849
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nes 95; Conservative
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                                                 24-SEP-1993;
24-SEP-1993;
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May 25, 2005, 17:25:01; Search time 11.8868 Seconds (without alignments) 596.600 Million cell updates/sec
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Sequence 3, A
Sequence 5, A
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-387-418A-14
US-09-387-418A-14
US-08-365-796-12
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US-08-956-653A-12

Sequence 9, Appli Sequence 8, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 14, Appli Sequence 14, Appl Sequence 14, Appl Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli	MENTS  IFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR  418A  477; DB 3; Length 95;  MO. 3.8e-45;  atches 0; Indels 0; Gaps 0;  QGDMQDLNGNNQSVTRQKWQQLEQMLTALDQMR 60  DWKRRPEI 95	18A ia H IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
770 1 US-08-416-581B-9 770 3 US-09-012-710-8 770 3 US-09-056-573-8 770 3 US-09-556-273-8 770 4 US-09-972-800A-6 771 1 US-08-72 771 1 US-08-72 771 1 US-08-78 771 1 US-08-78 772 1 US-08-78 774 1 US-08-78 778 3 US-09-38-418A-23 748 1 US-08-839-164-2 748 1 US-08-839-164-2 748 1 US-09-087-465-8 749 1 US-09-087-465-8 749 1 US-09-087-465-8 749 1 US-08-839-164-8 749 1 US-09-087-865-8 749 2 US-08-832-091-8 749 2 US-08-852-091-8 749 3 US-08-852-091-8	Melissa H Melissa H Masames E OS FOR IDENT ACTIONS : US/09/387, -08-31 .0 (0; Score 0; Pred. 0; Mism DDPDFNYKTLKS DDPDFNYKTLKS DDPDFNYKTLKS UNIMM	on US/093874 aokui nska, Meliss Curt M ETHOUS FOR INTERACTIONS INTERACTIONS 1999-08-31 43
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	ULT 1  equence 21, Application US, atent No. 6391572  atent No. 6391572  atent No. 6391572  APPLICANT: Arzeszczynska, APPLICANT: Horvath, Curt JAPPLICANT: Horvath, Curt JAPPLICANT: Darnell Ur., UTITLE OF INVENTION: INTERFERENCE: 600-1-253  CURRENT FILING DATE: 1999  NUMBER OF SEQ ID NOS: 43  SOFTWARE: PATENCE: PATENT NUMBER  EQ ID NO 21  EMOUTH: 95  TYPE: PRT  ORGANISM: MUS MUSCULUS  09-387-418A-21  1 VODLEOKMKVVENLO)  1 VODLEOKMKVVENLO)  61 RSIVSELAGLISAME:  61 RSIVSELAGLISAME:  61 RSIVSELAGLISAME:	ULT 2  99-387-418A-20 equence 20, Application US, atent No. 6391572 atent No. 6391572 APPLICANT: Zhang, Xiaokui APPLICANT: Wizeszczynska, APPLICANT: Horvath, Curt NAPPLICANT: Darnell Ur. JETILE OF INVENTION: INTERFETILE REFERENCE: 600-1-253 CURRENT APPLICATION UMBER: CURRENT RILING DATE: 19999-
28 466 29 466 31 466 33 466 34 466 36 37 466 38 39 466 36 466 466 466 466 466 466	RESULT 1  US-09-387-418A-21 Sequence 21, Applica Sequence 21, Applican Sequence 21, Applican Sequence 21, Sequ	RESULT 2 US-09-387-418A-20 US-09-387-418A-20 Sequence 20, Applica Patent No. 6391572 GENERAL INFORMATION: APPLICANT: WIZEGZC APPLICANT: HOTVATH APPLICANT: HOTVATH APPLICANT: Darnell TITLE OF INVENTION: CURRENT APPLICATION: CURRENT APPLICATION CURRENT APPLICATION UMBER OF SEQ ID NO
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Length 176; Indels

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Sequence 19, Application US/09387418A

Sequence 19, Application US/09387418A

Sequence 19, Application US/09387418A

Sequence 19, Application US/09387418A

APPLICANT: Zhang, Xiaokui

APPLICANT: Aresezzynska, Melissa H

APPLICANT: Horvath, Curt M

APPLICANT: Darnell Jr., James E

TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-1-253

CURRENT APPLICATION NUMBER: US/09/387,418A

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOPTWARE: PatentTr. V.-
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100.0%; Score 477; DB 3;
Best Local Similarity 100.0%; Pred. No. 8.2e-45;
Matches 95; Conservative 0; Mismatches 0;
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curr M
APPLICANT: Horvath, James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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US-09-387-418A-19
                                  ; ORGANISM: Mus musculus
US-09-387-418A-16
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APPLICANT: Wrzesczynska, Melissa H
APPLICANT: Wrzesczynska, Melissa H
APPLICANT: Wrzesczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-533
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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APPLICANT: Wrzeszczyneka, Melissa H
APPLICANT: Wrzeszczyneka, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
APPLICANT: Darnell Jr., James E
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APPLICANT: Marked Melissa H
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CURRENT APPLICATION NUMERR: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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; Sequence 16, Application US/09387418A
Patent No. 6391572
; GENERAL INFORMATION:
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   SOFTWARE: PatentIn Ver. 2.0
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CORGANISM: Mus musculus
US-09-387-418A-17
                                                                                                                                               ; ORGANISM: Mus musculus
US-09-387-418A-20
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SEQ ID NO 16
LENGTH: 176
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LENGTH: 143
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TYPE: PRT
                                          SEQ ID NO 20
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APPLICANT: Zhang, Xiaokui
APPLICANT: Areascaynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell JJr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
FILE REFERENCE: 600-1-253
CURRENT APPLICATION VUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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100.0%; Score 477; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                             86 RSIVSELAGILSAMEYVQKTLTDEELADWKRRPEI 120
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Pred. No. 1.1e-44;
                                                                                                                               61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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Best Local Similarity 100.0%; Pred. No. 1.1
Matches 95; Conservative 0; Mismatches
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                               Sequence 29, Application US/09387418A Patent No. 6391572 GENERAL INFORMATION:
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APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDEN
TITLE OF INVENTION: INTERACTIONS
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; Sequence 30, Application US/09387418A
; Patent No. 6391572
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Conservative
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; ORGANISM: Mus musculus
US-09-387-418A-29
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SEQ ID NO 29
TRNGTH: 229
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GENURAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Arzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: 1NTERACTIONS
TITLE OF LIVERTION: 105/09/387,418A
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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: UNMER: US/09/387,418A
CURRENT APLICATION UNMER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 229
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               Query Match
100.0%; Score 477; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0;
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0; Mismatches
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Best Local Similarity 100.
Matches 95; Conservative
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ORGANISM: Mus musculus
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Best Local Similarity
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SEQ ID NO 18
LENGTH: 229
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IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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100.0%; Pred. No. 1.4e-44;
:ive 0; Mismatches 0;
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100.0%; Pred. No. 1.3e-44;
ive 0; Mismatches 0;
                                    109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
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    61 RSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
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APPLICANT: Zhang, Xiaokui
APPLICANT: Horvach, Curt M
APPLICANT: Horvach, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ. ID NOS: 43
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curk
APPLICANT: Horvath, James E
APPLICANIVINATION: METHODS FOR IDENTIFYING
ITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                     Sequence 14, Application US/09387418A; Patent No. 6391572; GENERAL INFORMATION:
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95; Conservative
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Best Local Similarity 100.
Matches 95; Conservative
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ORGANISM: Mus musculus
US-09-387-418A-14
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SEQ ID NO 9
LENGTH: 271
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Sequence 31, Application US/09387418A

Patent No. 6391572

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui

APPLICANT: Darnell Jr., James E

APPLICANT: Darnell Jr., James E

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

CURRENT APPLICATION NUMBER: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09387418A

Sequence 15, Application US/09387418A

Patent No. 6391572

GRNERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Aresezcaynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: HORVATION: NETHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ. ID NOS: 43
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Best Local Similarity 100.0
Matches 95; Conservative
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RESULT 12

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SEQUENCE 12 Application US/08369796

SEQUENCE 12 Application US/08369796

SEQUENCE 12 Application US/08369796

SEQUENCE 12 US/08/1004

SEQUENCE 12 US/08/1004

SEQUENCE 12 US/08/1008

COMPUTER READBLE FORM:

WINDER PROPER 1 US/08/1008/1008

COMPUTER READBLE FORM:

WORDIN TYPE 1 Read PC COMPARIAN

COMPUTER READBLE FORM:

WORDIN TYPE 1 US/08/1008

SEQUENCE 1 US/08/1008

SEQUENCE
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Search completed: May 25, 2005, 17:47:37
Job time : 15.8868 secs

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May 25, 2005, 17:36:58; Search time 41.6038 Seconds (without alignments) 763.830 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Appl												
	_	21,	20,	17,	16,	19,	22,	18,	28,	29,	30,	31,	15,	14,
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
	ID	US-10-090-185-21	US-10-090-185-20	US-10-090-185-17	US-10-090-185-16	US-10-090-185-19	US-10-090-185-22	US-10-090-185-18	US-10-090-185-28	US-10-090-185-29	US-10-090-185-30	US-10-090-185-31	US-10-090-185-15	US-10-090-185-14
	DB	13	13	13	13	13	13	13	13	13	13	13	13	13
	Query Aatch Length DB	95	128	143	176	213	223	229	229	229	229	229	236	252
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	477	477	477	477	477	477	477	477	477	477	477	477	477
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Sequence 9, Appli Sequence 12, Appl Sequence 12, Appl Sequence 2, Appli Sequence 5, Appli	Sequence 8, Appli Sequence 5, Appli Sequence 2, Appli Sequence 329, App Sequence 349, App Sequence 780, App Sequence 780, App	Sequence 23, Appl Sequence 437, App Sequence 439, App Sequence 300, Appl Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli	Sequence 39, Appli Sequence 4, Appli Sequence 4, Appli Sequence 12, Appli Sequence 12, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 5, Appli
13 US-10-090-185-9 11 US-09-876-773-12 17 US-10-639-617-12 15 US-10-380-020-4 15 US-10-380-020-5 15 US-10-380-020-5	14 US-10-045-792-8 14 US-10-038-010-56 14 US-10-117-087-2 15 US-10-116-275-329 15 US-10-116-275-349 9 US-09-925-302-780	13 US-10-090-185-23 14 US-10-177-223-437 14 US-10-177-293-439 16 US-10-755-889-362 16 US-10-755-889-362 9 US-09-833-205-6 11 US-09-876-773-8 14 US-10-045-792-7	14 US-10-205-194-39 17 US-10-639-617-8 9 US-9-833-205-4 14 US-10-045-792-9 13 US-10-090-185-12 14 US-09-875-120-3 11 US-09-876-773-6 14 US-10-245-120-2 17 US-10-936-390-5 9 US-09-833-205-2
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## ALIGNMENTS

Sequence 21, Application US/10090185; Publication No. US20020197647A1; GENERAL INFORMATION:

JS-10-090-185-21

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GENERAL INFOGRATION:
CHARLA INFOGRATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Barnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SQFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 21
LENGTH: 95
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ORGANISM: Mus musculus
US-10-090-185-21
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Best Local Similarity
Matches 95; Conserv
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US-10-090-185-19

US-10-090-185-19

Sequence 19, Application US/10090185

Sequence 19, Application US/10090185

Sequence 19, Application US/20020197647A1

Sequence 19, Application No. US20020197647A1

APPLICANT: Wrzeszczynska, Melissa H

APPLICANT: Wrzeszczynska, Melissa H

APPLICANT: Horvath, Curt M

APPLICANT: Darnell Jr., James E

TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-1-253

CURRENT APPLICATION UNDER: US/10/090,185

CURRENT FILING DATE: 1202-03-04

PRIOR APPLICATION UNDER: 09/387,418

PRIOR FILING DATE: 1999-08-31

WUMBER OF SEQ ID NOS: 43

SEQ ID NOS: 43

SEQ ID NO 19

SEQ ID NO 19
                                                                                                                                                                                                                       IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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1 Similarity 100.0%; Pred. No. 4.8e-42;
95; Conservative 0; Mismatches 0;
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          US-10-090-185-16
Sequence 16, Application US/10090185
Sequence 16, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Chang, Xiaokui
APPLICANT: WIZESZCZYNSKA, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Mus musculus
US-10-090-185-16
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Best Local Similarity
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Best Local
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APPLICANT: Zhang, Xiaokui
APPLICANT: Areasczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curr M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR F
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INVERTOR: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                          APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR ITILE OF INVENTION: INTERACTIONS
FILE REPERBNCE: 600-1-253
CURRENT FILING DATE: 2002-03-04
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SEQ ID NOS: 43
SEQ ID NO 20
LENGTH: 128
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2.6e-42;
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ilarity 100.0%; Pred. No. 2
Conservative 0; Mismatche
                    Sequence 20, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
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Publication No. US20020197647A1
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US-10-090-185-20
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Best Local Similarity
Matches 95; Conserv
US-10-090-185-20
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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Horvath, Cut M
APPLICANT: Horvath, James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
PRIOR TELLING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Horvath, Cut M
APPLICANT: Horvath, James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
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100.0%; Pred. No. 5.3e-42;
tive 0; Mismatches 0;
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                                                                                                                                                            ; Sequence 28, Application US/10090185; Publication No. US20020197647A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/10090185; Publication No. US20020197647A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 229
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.
Matches 95; Conservative
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; ORGANISM: Mus musculus
US-10-090-185-28
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LENGTH: 229
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Publication No. US20020197647A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wizeszczynska, Melissa H
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 229
                                                                                                                                                                                                     APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Barnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REPERBACE: 600-1-23
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTHARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 223
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86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                                                                                           Sequence 22, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 95; Conservative
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Best Local Similarity 100.
Matches 95; Conservative
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US-10-090-185-22
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; ORGANISM: Mus musculus
US-10-090-185-18
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US-10-090-185-14

i Sequence 14, Application US/10090185

j Publication No. US20020197647A1

i GENERAL INFORMATION:

j APPLICANT: Talong, Xiaokui

j APPLICANT: Mrzeszczynska, Melissa H

APPLICANT: Horvath, Curt M

j APPLICANT: Naries FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

j TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

j TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

j FILE REPERENCE: 600-1-253

j CURRENT FILING DATE: 2002-03-04

j PRIOR FILING DATE: 1999-08-31

j NUMBER OF SEQ ID NOS: 43

s SOFUMANE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 477; DB 13; Best Local Similarity 100.0%; Pred. No. 5.5e-42; Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 RSIVSELAGLISAMEYVQKTLTDBELADWKRRPEI 143
                                         61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
              61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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; Sequence 31. Application US/20020197647A1
; Publication No. US20020197647A1
; Publication No. US20020197647A1
; Publication No. US20020197647A1
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
TITLE OF INVENTION: INTERACTIONS
; TITLE OF INVENTION: INTERACTIONS
; TITLE OF INVENTION: INTERACTIONS
; TITLE OF INVENTION: UNTERACTIONS
; TITLE OF INVENTION: UNTER: US010/090,185
; CURRENT FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR PLILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NOS: 43
; SEQ ID NOS: 43
; SED ID NOS: 2.0
                                                                                                                                           Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INPORMATION:
APPLICANT: Zhang, Xiackui
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR APLICATION NUMBER: 09/387,418
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-30
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100.0%; Pred. No. 5.3e-42;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                             61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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Matches 95; Conservative
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                                                                                                             RESULT 10
US-10-090-185-30
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155 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 100.0%; Score 477; DB 11; Length 770; Local Similarity 100.0%; Pred. No. 2.4e-41; les 95; Conservative 0; Mismatches 0; Indels 0
                                                                                                     FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Eq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21,5 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                     FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: May 25, 2005, 18:21:48
Job time : 53.9371 secs
                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEX: 133521
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Matches
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: WINBER: US/10/090,185
CURRENT PILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
49 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VQDLEQKWKVVENLQDDFDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR 60
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TITLE OF INVENTION: RECUENTION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
                                                                                  109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEL 143
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                                                     61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 477; DE
; Pred. No. 6.5e
0; Mismatches
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APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
                                                                                                                                                                                                                               Sequence 9, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 95; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wen, Zilong
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                               RESULT 14
US-10-090-185-9
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LENGTH: 271
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Gaps

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May 25, 2005, 17:24:07 ; Search time 8.96226 Seconds (without alignments) 1019.898 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                         OM protein - protein search, using sw model
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Title:	US-10-090-185-21
Perfect score:	477
Sequence:	1 VQDLEQKMKVVENLQDDFDFYVQKTLTDEELADWKRRPE
Scoring table: BLOSUM62	BLOSUM62
Gapop 10	Gapop 10.0 , Gapext 0.5

95

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

seq length: 0 seq length: 200000000 Post-processing: Minimum DB Maximum DB

Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote hypothetical prote 364K Golgi complex hypothetical prote transcription acti mammary gland fact hypothetical prote prote huma gamma-interferon a prote prote prote chain nypothetical prote prote interferon-depende prote kinesin-related pr coiled coil protei DNA-binding protei crystal ISGF3 p91-related orobable membrane epidermal growth mammary gland mammary qland tpr protein hypothetical hypothetical hypothetical hypothetical myosin heavy hypothetical hypothetical hypothetical Description parasporal SUMMARIES 149508 A56047 A46159 149274 T01613 S67087 A54444 554772 55557 24728 373852 AC2354 367605 40589 AD1029 302317 C5837 371203 871902 505697 58691 Ωï DB Query Match Length 638 1968 1160 304 76.5 76 75.5 75.5 75 75 85.5 84.5 84.5 83.5 82 81.5 79.5 466 466 1164 1158 93 93 88 88 77.5 Result Š.

heavy	myosin heavy chain	myosin heavy chain	peptidoglycan lyti	transmembrane prot	hypothetical prote	myosin heavy chain	myosin ii - fissio	interaptin - slime	cis-Golgi matrix p	cytoplasmic linker	hypothetical prote	centrosome autoant	troponin I - sea s	apolipoprotein A-I	apolipoprotein A-I
S03166	S07537	S10450	AC1763	AG1739	E71606	151302	T41522	T14867	T10754	T42734	T22976	A54103	JC5610	JC1237	S22420
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1979	412	621	398	927	980	764	1526	1738	986	1046	1133	2024	173	262	264
15.6	15.5	15.5	15.4	15.4	15.4	15.3	15.3	15.3	15.2	15.2	15.2	15.2	15.1	15.1	15.1
74.5	74	74	73.5	73.5	73.5	73	73	73	72,5	72.5	72.5	72.5	72	72	72
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C,Accession: A54444

C,Accession: A54444

S, Nahio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994

A,Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr
A,Reference number: A54444; MUID:94208062; PMID:7512451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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DNA-binding protein APRF - human
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:158950
A;Map position: 17421-17421
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
C;Generics:
A;Gene: GDB:STAT3; APRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 466; DB 2;
Pred. No. 1.3e-31;
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Best Local Similarity
                                                                                                                                                                                                          A; Accession: A54444
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ISGR3 p91-related transcription factor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: O2-Uul-1996 #sequence\_revision O2-Uul-1996 #text\_change O9-Jul-2004 C;Accession: I49508; I49009 R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su Cell 77, 63-71, 1994 A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr A;Reference number: A54444; MUID:94208062; PMID:7512451 RESULT 2

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES;
A;Cross-references: UNIPROT:P42227; GB:L29278; NID:g476715; PIDN:AAA37254.1; PID:g47671
B;Raz, R.; Durbin, J.E.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994

chromosome-associa

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NiAlternate gland factor - mouse
NiAlternate names: stat5 protein
C;Species: Mus musculus (house mouse)
C;Species: 27-Oct-1.95 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Jaccession: S54772; 149273
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-786 <RES>
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                            Query Match
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R;Schindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1987
A;Title: Proteins of transcription factor ISGF-93. one gene encodes the 91-and 84-kDa ISG
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA
A,Residues: 1-748 <YAM>
A,Cross-terneces: UnTRROT:P42228; GB:U09351; NID:g509502; PIDN:AAA19692.1; PID:g509503
C,Superfamily: human signal transducer and transcription activator STAT5A
C,Keywords: DNA binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
A,Title: Acute phase response factor and additional members of the interferon-stimulated
A,Reference number: 149009; MUID:95014185; PMID:7523373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rymanoto, K.; Quelle, F.W.; Thierfelder, W.B.; Kreider, B.L.; Gilbert, D.J.; Jenkins, Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Statt, a novel gamma interferon activation site-binding protein expressed in et A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                        9
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C;Species: Mus musculus (house mouse)
C;Date: 19-Oct_1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 VÓDLEQKMKVVENLÓDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                         A;Accession: I49009
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-393, M',395-700,702-770 <RE2>
A;Residues: 1-393, M',395-700,702-770 <RE2>
A;Cross-references: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890
C;Genetics: ApRF
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                        1 VODLEQKMKVVENLODDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
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C;Superfamily: human signal transducer and transcription activator STAT5A
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                                                                                                                                                                                                                                                                                                        Length 770;
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                                                                                                                                                                                                                                                                                                        'Match 97.7%; Score 466; DB 2; Length 77 Local Similarity 97.9%; Pred. No. 1.3e-31; Locals 1; Indels les 93; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 MRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
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Best Local Similarity 35.18
Matches 34; Conservative
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R; Yamamoto, K.; Quel
Mol. Cell. Biol. 14,
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A,Cross-references: UNIPROT:P42232; UNIPROT:Q9JKM1; EMBL:U21110; NID:g747973; PIDN:AACS R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A. Brando, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A. A. 116.1175, 1995
A;Title: Interleukin.3, granulocyte-macrophage colony stimulating factor and interleuki A;Reference number: S54772; MUID:95237198; PMID:7720707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-treferences: BMBL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
A; Cross-treferences: BMBL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R; Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris, BRBO J. 14, 1402-1411, 1995
A; Title: Interleukin-3 signals through multiple isoforms of Stat5.
A; Reference number: S54725; MUID:95246733; PMID:7537213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: STATS protein homolog p80
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49274; SS4773; SS4727
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8813-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved
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                                                                                                                                                       2 ODLEOKWKVVENLODDFDFNY-KTLKSOGDMODLNGNN-----OSVTROKMQQLEOML 53
                                                                                                                    9
                                                                                                                 1 VQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
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C;Superfamily: human signal transducer and transcription activator STAT5A
                                                           Gaps
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33.1%; Score 158; DB 2; 36.2%; Pred. No. 8.9e-06; iive 22; Mismatches 36,
                                                                                                                                                                                                                                                                               I 9.5%; Score 93; DB 2; Local Similarity 26.4%; Pred. No. 2.7; nes 28; Conservative 10. William
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A;Molecule type: mRNA
A;Residues: 1-432,'E',434-786 <AZA>
                                                                  34; Conservative
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A, Residues: 1-794 <MAK>
A, Residues: 1-794 <MAK>
A, Cross-references: UNIPROT: P42231; EMBL: X78428; NID: g602354; PIDN: CAA55191.1; PID: g602
A, Note: this is a revision to the sequence from reference 544353
R; Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A; Title: Mammary gland factor (WGF) is a novel member of the cytokine regulated transcr
A, Reference number: S44353; MUID: 94244619; PMID: 7514531
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C;Date: 22-Nov-1993 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C;Date: 22-Nov-1993 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C;Accession 533124; S23740; $\frac{2}{3}00928; G01185
R;Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 2329-2333, 1992
Oncogene 7, 2329-2333, 1992
A;Title: The human tpx gene encodes a protein of 2094 amino acids that has extensive co A;Reference number: $33124; MUID:93064711; PMID:1437155
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Best Local Similarity
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                                         A; Accession: 33.7.6.
A; Accession: 33.7.6.
A; Accession: 1.793 A; Accession: 51.70.
A; Accession: 1.793 A; Accession: 52.7.6.
A; Accession: 1.793 A; Accession: 1.793
        Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
Reference number: S54772; MUID:95237198; PMID:7720707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g115
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
R;Accession: S5527; 84353
EMBO J. 14, 854-855, 1995
BMEO J. 14, 854-855, 1995
A;Title: Corriganda. Mammary gland factor (MGF) is a novel member of the cytokine regula A;Reference number: S55527; MUID:95188889; PMID:7882987
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Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QDLEQKWKVVENLQDDFDFNY-KTLKSQGDMQDLNGNN-----QSVTRQKMQQLEQML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 QREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDDELIQWKRRQQL 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.5%; Score 93; DB 2; Length 793; 26.4%; Pred. No. 2.7; ive 18; Mismatches 48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997
C;Accession: G02317
R;Lin, J
Submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription activator stat5A - human
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Best Local Similarity 26.4%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mammary gland factor - sheep
Interleukin-3,
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C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72593
C;Accession: G72593
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
AyA Res, G, 83-101, 1999
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9YCP2; DDBJ:AP000061; NID:g5104821; PIDN:BAA80205.1; PID:d
A;Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: kinase-related transforming protein (tpr-met); protein with promoter
                                                                                                                                                                                                                                                                                                                 ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Э,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 ÓDTENELKKLÓGTÓEYFIIGYGESLRIGAGFAGLAGLNPGERLSRETALGGKGVSLEAWL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 VEDLEARVGSVEDRLSQAEEDIDSLTTSLDSLRTELEDLSTRLAEAQASLEDLÄTRLDQV 396
                                                                                                                                                                                                                                                                                                                                                                                        2 QDLEQKMKVVENLQDDFDFNY-KTLKSQGDMQDLNGNN-----QSVTRQKMQQLEQML 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- DPNYKTLKSQGDMQDLNGNNQSV
A;Molecule type: mRNA
A;Residues: 1-716, RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                  ch 18.4%; Score 88; DB 2; Length 794; 1 Similarity 27.2%; Pred. No. 7.2; 28; Conservative 16; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 533;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 QREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDDELIQWKRR 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 A-STLQQLQQRLATAEESLQALTEDLASLQAEVETLQQSIVE 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 TROKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 ----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR
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A;Residues: 1-821 <WIL>
A;Cross-references: UNIPROT:P45970; EMBL:Z36753; PIDN:CAA85342.1; GSPDB:GN00020; CESP:T<sup>o</sup>
A;Experimental source: clone T09A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364X Golgi complex-associated protein - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004 C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004 C;Date: 05-Mar-1998 #sequence_revision 15-Mar-1998 #text_change 09-Jul-2004 R;Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ikehara, Y. Cell Struct. Funct. 22, 565-577, 1997 A;Title: Identification and characterization of rat 364-kDa Golgi-associated protein replacement mumber: JCS837; MulD:98093490; PMID:9431462
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A;Molecule type: mRNA
A;Residues: 1-3187 <-TOK.
A;Cross-references: UNIPROT:Q63714; DDBJ:D25543; NID:g516825; PIDN:BAA05026.1; PID:g516
C;Comment: This protein plays a role in the formation and maintenance of the characteri
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F;49-549,624-1176,1238-1707,1763-3114/Domain: coiled-coil leucine zipper #status predic
F;3165-3187/Domain: membrane anchor #status predicted <MAD>
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                                                                                                                                                                                                                                                                                                         hypothetical protein T09AS.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.5%; Score 83.5; DB 2; Length 3187; Best Local Similarity 25.5%; Pred. No. 76; Matches 26; Conservative 17; Mismatches 40; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.9%; Pred. No. 15;
Matches 27; Conservative 22; Mismatches 31; Indels 33
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R. Lightning, J. Submitted to the EMBL Data Library, August 1994
A. Reference number: Z19928
A. Accession: T24728
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
                                                                                              60 RRSIVSELAGLLSAMEYVQKTLTDEELADWKRPPEI
132 LEELKRKVRRLEVLEDDFDHLKEQLIKQEGQLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 QLEQMLTALDQMRRSIVSELAGLLSAMEYV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 2
A; Introns: 47/2; 253/2; 604/3; 643/1; 712/3
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                                                                                                                                                                                                                                                      RESULT 12
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                                  A; Residues: 1-2094 - MIT>
A; Cross-references: UNIPROT: 015624; UNIPROT: 09UE33; EMBL: X66397; NID: 9633225
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
R; Mitchell, P.J.; Cooper, C.S.
A; Mitchell, P.J.; Cooper, C.S.
A; Recense number: $23740; MUID: 92195670; PMID: 1549355
A; Recense number: $23740; MUID: 92195670; PMID: 1549355
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-725, 'L' - MIZ>
A; Rilly; H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
A; Reference number: $00928; MUID: 88262257; PMID: 3387099
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A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB2166
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G75219
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome A;Reference number: A75001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GDMQDLNGNNQSVTRQKMQ 47
            A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: BMBL:X94208; NID:g1296797; PIDN:CAA63904.1; PID:g1296798 C;Genetics: A;Gene: GDB:TPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues: 1-31,'R',33-142 <KIN>
Cross-references: EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PID:g37256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1478 ELKETLNQAETKSKSLESQ-----VENLOKTLSEKE 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, December 1995 A; Reference number: H00592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 17.7%; Score 84.5; DE Similarity 24.0%; Pred. No. 3.6; 23; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 17.9%; Score 85.5; DE Best Local Similarity 26.5%; Pred. No. 33; Matches 26; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 DLEOKMKV---VENLQDDFDFNYKTLKSQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:128821; OMIM:189940
A;Map position: 1q25-1q25
A;Introns: 177/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 144-228 <GRE>
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A,Molecule type: DNA
A,Residues: 1-217 <KAW>
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A; Residues: 1-31,'R',3
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1 VQDLEQKMKVVENLQDDFD-FNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQM 59

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Ritimelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
Aritle: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A; Reference number: S73327; MUID:97105885; PMID:8948633
A; Accession: S73852
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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PH1895
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P75471; EMBL:AE000051; GB:U00089; NID:g1674211; PIDN:AAB9617
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
protein MG218 homolog F10_orf1818 - Mycoplasma pneumoniae (strain ATCC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekii M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch) MA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1291 VSELRĢEKKOLLSAĢKQVDDKSRLLEQNQRHLQNLS----SETKKKRQSLEHDINKFDQR 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 LEELKKKIRRLEVIEDDFDHLKEQLIKQEGQLE------MARRYIKLLEGVRHDIDNI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VQDLEQKMKVVENLQDDFDFNYKTL-KSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQM 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B71203
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                            iriety: ATCC 29342
ite: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: B71203
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                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1818 <HIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Genetics:
A,Genetic code: SGC3
C,Superfamily: Mycoplasma genitalium hypothetical protein MG218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 RRSIVS------ELAGLLSAMEYVQKTLTDEELA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.2%; Score 82; DB 1
ilarity 27.5%; Pred. No. 56;
Conservative 21; Mismatches
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Job time : 12.9623 secs
                                Species: Mycoplasma pneumoniae
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bucken, K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hateh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernath K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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                                                                                                 May 25, 2005, 17:15:30 ; Search time 39.5283 Seconds (without alignments) 1230.701 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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1: uniprot_sprot:*
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P42224 homo sapien Q68d00 homo sapien Q8jfu8 brachydanio Q8jgn0 xenopus lae Q7zz53 brachydanio					rs			ate)	annotation update) ator of transcription 3 (Acute-phase	•		Craniata; Vertebrata; Buteleostomi; Catarrhini: Hominidae: Homo			1016/00	Matsusaka T.,	3	n the gp130-mediated signaling			00 (	Pezzotti A., Serlupi-Crescenzi O.; semience between mirine STAT3 and a	1		VARIANT ILE-143.	., Hastings N.C., Ahearn M.O.,	genomic applications, UW-	(URL: http://pga.gs.washington.edu)."; ) to the EMBL/GenBank/DDBJ databases.		701).	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	L.H., Derge J.G.,
HUMAN 0 18 10					ALIGNMENTS	c t		e upda	ion up			ıata; rrhini			00T=10	×	shimot 1 IFN-	ved ir			001=10	cti A	i i		•		n for	a.gs.v		AND DEL-701)	DOI=1	nae r
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158 158 156 155	154 153.5 153	147	134	121		L (AN	P40763; 01491	01-FEB-1995 05-JUL-2004	25-OCT-2004 (Rel. Signal transducer	response factor)	Name=SIAIS; Synonyms=AFKF Homo sapiens (Human).	caryota; malia: F	NCBI_TaxID=9606;	SEQUENCE FF	TISSUE=Placenta; MEDITNE=94208062;	ra S., N	Yoshida K., Sudo T., l "Molecular cloning of	lated tra	Cell 77;63-71(1994)	DITENCE FE	MEDLINE=98296260; Pubmed=9630560; DOI	Della Pietra "Highly consf	revised hum	ne 213:11	SEQUENCE FROM N.A.	eder M.J.	attlesn	FHCRC, Seattle, WA (URL: http://pga. Submitted (MAR-2004) to the EMBL/Gen		SEQUENCE FROM N.A TISSUE=Kidney, an	OLINE=223	causberg
3333 35433 36433	3.3.4 3.9.8 3.9.8	044	1 4 4 4 1 W 4 11			.7 1	P4 (	9.5	25.	ě	Homo .	Eul Man	Ŋ.	SEO	TI	Ä	ž č	r e	S S	. [2]	W.	De.	re	Gene	SEC	Rit	រុំ ខ្លុ	Str	[4]	SEC	ME	St
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005737; C:cytoplasm; TAS.
GO:0005634; C:nucleus; TAS.
GO:0005662; F:hematopoietin/interferon-class (D200-domain. ..; TAS.
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COGRETATION: Transcription factor that binds to the interleukin-6
--- FUNCTION: Transcription factor that binds to the interleukin-6
--- FUNCTION: Transcription factor that binds to the interleukin-6
--- FUNCTION: Transcription factor that binds to the promoters of various (IL.6) -reapponaive elements identified in the promoters of various acute-phase protein genes.
--- FATHWAY: Involved in the gp130-mediated signaling pathway.
--- FATHWAY: FORMS a homodimer or a heterodimer with a related family member (at least STAYI). Interacts with NCOAI.
--- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
--- ALTERNATIVE PRODUCTS:
--- Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolda-P40763-2; Sequence-VSP 010474;
Isolda-P40763-2; Sequence-VSP 010474;
TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.

PIN: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.

SIMILARITY: Belongs to the transcription factor STAT family.

SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11773079; DOI=10.1074/jbc.M111486200;
Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
"Functional interaction of STAT3 transcription factor with the
coactivator NCoA/SRCIa.";
                                                                                                                                                                                                                                                                                                                                  MEDLINE=95215843; PubMed=7701321;
Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
"Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                   Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P40763-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ012463; CAA10032.1; -. EMBL; AY572796; AAS66986.1; -. EMBL; BC000627.1; -. EMBL; BC014482; AAH14482.1; -. EMBL; AF029311; AAB84254.1; -.
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                                                                                                                                                                                                            SEQUENCE OF 564-704 FROM N.A.
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                                                                                                                                             and mouse cDNA sequences.";
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TRANSFAC; T01493; -
Genew; HGNC:11364; STAT3.
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                                                                                                                                                                                                                                     TISSUE=Liver;
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MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
Yoshida K., Sudo T., Naruto M., Kishimoto T.;
"Molecular cloning of APRF, a novel IRN-stimulated gene factor 3 p91-
related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                          Phosphotyrosine (by JAK) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185 AND 632-640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VODLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                             InterPro; 1FR0/11; SH2; 1.
Pfam; PP00017; SH2; 1.
Pfam; PP01017; SH2 alpha; 1.
Pfam; PF02865; STAT int; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; Alternative splicing; DNA-binding; Nuclear protein;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
GO; GO:00003700; F:transcription recovered GO; GO:0006928; P:cell motility; TAS.
GO; GO:000728; P:JAK-STAT cascade; TAS.
GO; GO:0007129; P:negative regulation of transcription from P.
GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR008967; PS3_like_DNA_bnd.
InterPro; IPR001917; STAT.
InterPro; IPR001217; STAT.
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2.4e-31;
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P -> S (in Ref. 1).
F -> N (in Ref. 1).
F -> L (in Ref. 1).
T -> L (in Ref. 1).
T -> A (in Ref. 1).
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                                                                                                                                                                                                                                                                                                                      FTIG=VAR_018679
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SEOUENCE FROM N.A. (ISOFORM STAT3A)
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DOMAIN 580 670 SH
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AC P42227;
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SEQUENCE FROM N.A. (ISOFORM STAT3A).

STRAIN=FVEN, TISSUE-Mammary gland;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,

Altesnul S.F., Zeeberg B., Buerow K.H., Schamen C.M., Schuler G.D.,

Altesnul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan D.J., McKernan K.J., Maket J.A., Gunzarane P.H.,

Althards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roder B.D., Dickson M.S.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roder B.D., Dickson M.S.,

Roder B.D., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roder B.D., Dickson M.S.,

Roder B.D., Smailus D.E.,

Roder B.
                                                                                                                                                                MEDLINE-95014185; PubMed=7523373;
Raz R., Durbin J.E., Levy D.E.;
"Acute phase response factor and additional members of the interferon-stimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
                                Zhong Z., Wen Z., Darnell J.E. Jr.; "Stats: a STAT family member activated by tyrosine phosphorylation in response to epidernal growth factor and interleukin-6."; Science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.
MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
Wen Z., Zhong Z., Darnell J.E. Jr.;
"Maximal activation of transcription by Statl and Stat3 requires both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.,
"Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                                       Schaefer T.S., Sanders L.K., Nathans D.; "Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J, and NOD/LtJ;
Davoodi-Semiromi A., She J.-X.;
A mutant StatSb with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
MEDLINE=96016116; Pubmed=7568080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine and serine phosphorylation.";
Cell 82:241-250(1995).
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                     MEDLINE=94188718; PubMed=8140422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 71:150-155(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zebrafish to mouse.";
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TISSUE=Thymus;
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Three-dimensional structure of the Statibleth homodimer bound to RT. Three-dimensional structure of the Statibleth homodimer bound to RT. Three-dimensional structure of the Statibleth homodimer bound to RT. Three-dimensional structure of the Statible of the Statible of Various of the Past of University of Various of Citics). The Statible of the Statible of Citics of Citics
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ITCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various acute-phase protein genes.

PATHWAY: Involved in the gp130-mediated signaling pathway.
SMBUNIT: Forms a homodimer or a heterodimmer with a related family member (at least STATI). Interacts with NCOA1 (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
                                                                                                                                                                                                                                                                                                   1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                    Gaps
        FDMDLTSECATSPM -> FIDAVWK (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29999; Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F., Fey G.H.;
                                                                                                                                                                                                                                                                                   ;
0
                       /FTIG=VSP 006287.
Missing (in isoform Del-701).
/FTIG=VSP_010475.
S->A: Decreased transcriptional
                                                                                                                                                                                                                                                                97.7%; Score 466; DB 1; Length 770; 97.9%; Pred. No. 2.4e-31; Live 1; Mismatches 1; Indels
                                                                   E -> K (in Ref. 2).
S -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                      215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
                                                                                                                                                                                                                                                                                                                                      95
                                                                                                                                                                                                                                                                                                                                      61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                            activation.
                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                  727
                                                                                                                                                                                                                                                                         Local Similarity
les 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                    727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Stat3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elements."
                                                                                                                                                                                                                                                                                                                                                                                                 STA3 RAT
P52631;
                                                                   CONFLICT
CONFLICT
CONFLICT
HELIX
                                                                                                                                                                                                                                                                   Query Match
VARSPLIC
                                  VARSPLIC
                                                   MUTAGEN
                                                                                                                                                                                   HELIX
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HELIX
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HELIX
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                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P42227; 1BG1.

RGD; 3772; Stat3.

InterPro; IPR0008967; P53 like_DNA_bnd.

InterPro; IPR001217; STAT.

Pfam; PF00017; STAT alpha; 1.

Pfam; PF02864; STAT_blnd; 1.

Pfam; PF02864; STAT_blnd; 1.

Pfam; PF02865; STAT_int; 1.

SWART; SM00252; STAT_int; 1.

ROSITE; P550001; SH2; 1.

Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Mammary gland;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.,
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various acute-phase protein genes (By similarity).
-!- PATHWAY: Involved in the gp130-mediated signaling pathway.
                          PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, ILF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity (By similarity). SIMILARITY: Belongs to the transcription factor STAT family. SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
MCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphotyrosine (by JAK) (By
Phosphoserine (By similarity)
D74A0C76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL_2004 (Rel. 44, Created)
5-JUL_2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
response to phosphorylation (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       770 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X91810; CAA62920.1; -.
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match... 97.7
Best Local Similarity 97.9
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              727
770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=STAT3;
Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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.MOD_RES
SEQUENCE
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DLEQKWKVVENLQDDFDFNYKTLKSQ-DMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Mammary gland;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
GO: GO: GO: GO: GO: GENFORM TEA.
GO: GO: GO: GO: GO: F: transcription factor activity; IEA.
GO: GO: GO: GO: F: transcription factor activity; IEA.
GO: GO: GO: GO: F: transcription factor activity; IEA.
GO: GO: GO: GO: F: transcription of transcription, DNA-dependent; IEA.
InterPro; IPR001217; STAT.
NNN_TER
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BEDLINE-20107399, PubMed=10642787; DOI=10.1006/dbio.1999.9518;
Nishinakanura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
Asashima M., Yokota T.;
                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Signal transducer and activator of transcription 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.3%; Score 440.5; DB 2; Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12552 MW; 9961C28E59085803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92
                                                                                                           63 IVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
                                                                                       RSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            769 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                        108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog)
                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90; Conservative
                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                         Bovinae; Bos
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                                                                                       61
                                                                                                                       215
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                                                                                                                                                                                                        Q704W6
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Q9PVX8
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                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).
-!- SIMILARITY: Belongs to the transcription factor STAT family.
-!- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                       (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 VQDLEQKMKVVENLLDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMR
                                                                                                                                                                                                                                                                 PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou G.Y., Leung P.C.;

Zhou G.Y., Leung P.C.;

EMBL, AY641397, AAT64887.1, --

GO, GO:0005634; C:nucleus; IEA.

GO, GO:0004811; F:signal transducer activity; IEA.

GO, GO:000710; F:transcription factor activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR0009867; P33.1ike_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                   Phosphotyrosine (by JAK) (By si
Phosphoserine (By similarity).
9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   96.2%; Score 459; DB 1; Length 770; 96.8%; Pred. No. 9.4e-31; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.5%; Score 451; DB 2; Length 771;
94.7%; Pred. No. 4.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88174 MW; 71AC855C5DEC03E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal transducer and activator of transcription 3 Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sed
                                                                                                                                                                                                                                                   EMBL; AJ620655; CAF06182.1; -.
                                                                                                                                                                                                                                                                                                                                                                    770 AA; 87974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF01017; STAT alpha, 1.
PF02864; STAT bind, 1.
PF02865; STAT int; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.8°
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 94.7
Matches 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                   MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Gaps

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SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6DVF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
        ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA Straubberg R.D., Feingold E.A., Grouse L.H., Darge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
R. Brownstein M.J., Usdin T.B., Tooahlyuki S., Carninci P., Frange C.,
R. Brownstein M.J., Usdin T.B., Tooahlyuki S., Carninci P., Frange C.,
R. Brownstein M.J., Widnin T.B., Tooahlyuki S., Carninci P., Frange C.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 VQDLEQKAKVVENLQDDFDFNYKTLKSQSDLSELNGNNQSVTRQKMQQLEQMLTALDQLR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
        cytokine receptor gp130 ventralizes Xenopus
                                                                                                                                                                                          GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008867; PS3_like_DNA_bnd.
InterPro; IPR00980; SH2.
InterPro; IPR001717; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 432; DB 2; Length 769;
Pred. No. 1.9e-28;
7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50001; SH2; 1.
769 AA; 87974 MW; 0905C03263303069 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
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"Activation of Stat3 by cytokine embryos independent of BMP-4."; Dev. Biol. 216:481-490(1999).
EMBL: AB017701; BAR86061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84; Conservative
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                                                                                                                                                                  P42227; 1BG1.
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155 VQDLEQKAKKVVENLQDDFDFNYKTLKSQSDLSELNGNNQSVTRQKMQQLEQMLTALDQLR 214
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
SioCT-2004 (TrEMBLrel. 28, Last annotation update)
Signal transducer and activation of transcription factor 3.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR0009867; P53 like_DNA_bnd.
InterPro; IPR001217; STAT.
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                                                                                                                      'Genetic and genomic tools for Xenopus research: The NIH Xenopus
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MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
KIein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO447117; AAH44717.1; -.
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        766 AA; 87599 MW; 31018A3321CCEB9C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 427; DB 2;
Pred. No. 5e-28;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02865; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SWART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
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                                                                                                                                                                                                    Dev. Dyn. 225:384-391(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83; Conservative
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Best Local Similarity
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                                                                                                                                                                       initiative.";
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Local Similarity
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                                                                                                       1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLNGNNQ-SVTRQKMQQLEQMLTALDQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VQDLEQKAKVVENLQDDFDFNYKTLKSQGDM-QDLNGNNQ-SVTRQKAQQLEQMLTALDQ 58
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Gaps
                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation 3 isoform 1.
07-yzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Wertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                Liu R., Hong Y.;
Submitted (NAX-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY641434; AAT4654.1; -
GO, GO:0005634; C:nucleus; IEA.
GO, GO:0004871; F:signal transducer activity; IEA.
GO, GO:000770; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008967; P3_like_DNA_bnd.
InterPro; IPR001217; STAT.
                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

79.9%; Score 381; DB 2; Length 785;
Best Local Similarity 77.3%; Pred. No. 4.2e-24;
Matches 75; Conservative 14; Mismatches 6; Indels
                                                         79.9%; Score 381; DB 2; Length 765; 77.3%; Pred. No. 4.1e-24;
                                                                                Indels
                              765 AA; 87566 MW; P5D01408748EC703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50001; SH2; 1.
SEQUENCE 785 AA; 89643 MW; 81F231BDB27DE938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                250
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                                                                                                                                                    59 MRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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LRRQIVTEMGGLLTAMDYVQKNLTDEELADWKRRQQI
                                                                                                                                                                                                                                    785 AA.
                                                                      ; Pred. No. 4.1e
14; Mismatches
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                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01017; STAT alpha; 1. Pfam; PF02864; STAT bind; 1. Pfam; PF02865; STAT int; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PKOSITE; PS55001; SH2; 1.
SEQUENCE 765 AA; 87566 MW
                                                  Query Match
Best Local Similarity 77.3%;
Marches 75; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      072TS5;
01-07N-2003 (TEMBLrel. 24,
01-07N-2003 (TEMBLrel. 26,
01-MAR-2004 (TEMBLrel. 26,
                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8090;
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Q7ZTS5
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STRAIN=AB; TISSUE=Whole body;

RA STRAIN=AB; TISSUE=Whole body;

RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibeh F.,

RA Brownstein M., Soares M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Widin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McKwan P.J., McKernan R.J., Malk J.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Raphy J., Helton B.K., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rhodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rodersation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VQDLEQKMKVVENLQDDPDPDPNYKTLKSQGDM-QDLNGNNQ-SVTRQKMQQLEQMLTALDQ
------y-auno rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Weopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBL_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005634; C:nucleus; IRA.
GO; GO:0004871; P:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0005155; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR00967; P33 like_DNA_bnd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRANIF=AB; TISSUE=Whole body;
Straniberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; PGC045276; AAH45276.1; -.
ZFNN; ZDB-GENB-980526-68; stat3.
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PF02864; STAT_bind; 1.
PF02865; STAT_int; 1.
NCE 414 AA; 48253 MW; 0FFD1BS09B7526BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 LRRQIVTEMAGLLSAMDFVQKNLTDBELADWKRRQQI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.5%; Score 379; DB 2; 77.3%; Pred. No. 3.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 MRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequences.";
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                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MISTAURDER R.D., Colling F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
MARUSINE R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brapleron M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
M. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodriques S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mriting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;

R. Mannes M. M. Initial malysis of more than 15,000 full-length human M. Mannes Physic R.M.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR0009867; PS3_like_DNA_bnd.
InterPro; IPR00980; SI3_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO68320; AAH68320.1; -.
ZFIN; ZDB-GENE-980526-68; stat3.
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Last annotation update)
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Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad.
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=stat3;
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                        SO DER RESERVACIONES DE LA PRESERVACIONES DE LA PRE
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                                                                                                                                                                                                                                                                                                   R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0004871; F:signal transducer activity; IEA.

R GO:0007242; P:intracellular signaling cascade; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000967; P53_like_DNA_bnd.

R InterPro; IPR000967; SH2:.

R Pfam; PF0001017; SH2:.

R Pfam; PF001017; SH2:.

R Pfam; PF001017; STAT alpha; 1.

R Pfam; PF02864; STAT alpha; 1.

R Pfam; PF02865; STAT bind; 1.

R R MART; SM00252; SH2: 1.

R PROSITE; PS50001; SH2: 1.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006352; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008967; P53_like_DNA_bnd.
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Butaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygi; Neopterygi; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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Johnson M.C., Mourich D.V., Leong J.C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U60333; AAB60926.1; -.
HSSP; P42227; 1BG1.
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Last annotation update)
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                                                                                                                                             SEQUENCE FROM N.A.
Oates A.C.;
Thesis (1998), University of Melbourne, Australia.
Embl., AJO05693; CAA06677.1; -.
HSSP, P42227; 1BG1.
ZFIN; ZDB-GENE-980526.68; Stat3.
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02865; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
SEQUENCE 767 AA; 87816 MW;
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                                                              1 VQDLEQKAKVVENLQDDFDFNYKTLKSQGDM-QDLNGNNQ-SVTRQXAQQLEQMLTALDQ
                                 Gaps
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
Pfam; PF00017; SH2; 1.
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78.4%; Score 374; DB 2; Length 764;
Best Local Similarity 76.3%; Pred. No. 1.6e-23;
Matches 74; Conservative 14; Mismatches 7; Indels
    Length 767;
                                 Indels
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307106; AAL09415.1; -.
HSSP; 942227; 18G1.
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; 87411 MW; E661FFE18BEFD8BE CRC64;
                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                            Ouery Match 78.6%; Score 375; DB 2; L
Best Local Similarity 75.3%; Pred. No. 1.3e-23;
Matches 73; Conservative 17; Mismatches 5;
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Abu04735 Human e Abu04745 Human e Abu04743 Human e

Perfect score:

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Sequence:

Scoring table:

Searched:

Database

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The present sequence is mouse Stat3 protein fragment containing 249-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-un and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A
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94. :110
34. et stata c-Jun interaction region 2; corresponds to
342-358 position of Stata protein"
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AAY72860
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0; Mismatches

Score 669; DB 4; Pred. No. 6.8e-69;

100.0%; 100.0%;

В

Length 185; Indels 116

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IVELFRNLMKSAFVVERQPCMPWHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
                                                                                                                                                                             Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                  1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse Stat3 protein fragment #12 (155-377 amino acids)
                                                                                                                                                                                                                                                                                                                                             AAY72854 standard; protein; 223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2000; 2000WO-US023822
                                Query Match 100.
Best Local Similarity 100.
Matches 129; Conservative
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                                                                                                                                                                                                                              DKDSGDVAA 129
                                                                                                                                                                                                                                                              DKDSGDVAA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-226705/23.
Sequence 185 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                            177
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                                                                                                                                                                                                                 61 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPBLNYQLKIKVCI 120
                                                                                                                                                                                                                                  The present sequence is mouse Stat3 protein fragment containing 193-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriais. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                        IACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                  1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
 Stat protein comprises the N-terminal domain, coiled-coil domain, DNR binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein:
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0
                                                                                  Length 129;
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse Stat3 protein fragment #13 (193-377 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Darnell JE;
                                                                                  100.0%; Score 669; DB 4;
100.0%; Pred. No. 4.2e-69;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                AAY72855 standard; protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 65; Page 80; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-AUG-2000; 2000WO-US023822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00387418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                    Matches 129; Conservative
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                                                                                                                                                                                                                                                                                 DKDSGDVAA 129
                                                                                                                                                                                                                                                                                                       DKDSGDVAA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226705/23.
                                                                                                 Local Similarity
                                                     Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200116605-A2
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                                                                                       Ouery Match
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188. .204 /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"

Location/Qualifiers

(first entry)

E)

Darnell

Wrzeszcynska MH,

99US-00387418

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The present sequence is mouse Stat3 protein fragment containing 155-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                        Claim 65; Page 79; 86pp; English.
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Length 271;

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us-10-090-185-24.rag

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Similarity
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                                            129;
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                 Query Match
Best Local &
                               Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                           Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                      1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Stat3-c-Jun interaction region 2; corresponds 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                            Indels
                                                                                                                                                                                                                                                                                                                                                Mouse Stat3 protein fragment #2 (107-377 amino acids).
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            Pred. No. 8.7e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wrzeszcynska MH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                            AAY72841 standard; protein; 271 AA.
100.0%; Pre-
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                            Conservative
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                                                                                                                                                                                   DKDSGDVAA 223
                                                                                                                                                                 DKDSGDVAA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-226705/23
            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-1999;
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                                                                                                                                                                                             215
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                                                                                                                                                                                                                                                                                                                                                                                                       therapy.
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Region
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Sequence 271 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
                                                                                                                                         1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                 143 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypozia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; drave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative diseorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative diseorder; lesion; Statbeta.
                                    Gaps
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                                    Indels
100.0%; Score 669; DB 4;
100.0%; Pred. No. 1.1e-68;
ilve 0; Mismatches 0;
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/note= "Encoded by ACA CCA TTC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                      AAE22055 standard; protein; 720
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                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Stat3beta protein.
                                                                                                                                                                                                               DKDSGDVAA 129
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tissue ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, tranuma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, critogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, crydematosus, multiple sclerosis, insulin dependent diabetes mellitus, crydematosus, multiple sclerosis, insulin dependent diabetes mellitus, crydematosus, sulcinamy biliary cirrhosis, pernicious mixed connective tissue disease, primary biliary cirrhosis, pernicious cracainoma, autoimmune purpura, drave's disease, valuematoid arthritis, diapethic Adaison's disease, valuematoid arthritis, cirrhosis, pemphygus vulgaris, autoimmune crifity, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating carcinomas e.g., bladder carcinoma, colon carcinoma, chomose e.g., bladder carcinoma, colon carcinoma, cromas and carcinoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human cross at the present sequence is human cross and carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 669; DB 5; Length 720; 100.0%; Pred. No. 4.2e-68; cive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB57164 standard; protein; 769 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-034733/04.
N-PSDB; ABI99454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stat3beta protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 720 AA;
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample comprising the expression profile of a gene group in the sample comprising selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB19202 to AB19912), encoding the protein sequences in ABB5702 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 IACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
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      by measuring
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           Examining the ischemic condition (e.g. occlusive ischemia) by measurin expression levels of particular genes defined in the specification or determining the expression profile of a gene group comprising these
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100.0%; Score 669; DB 5;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0;
                                                                                                                     Claim 2; Page 1084-1087; 2690pp; English.
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ng angiogenesis and an immune response in an individual, for
a hypoxic or ischemic condition, comprises administering a
that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                               dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and
                                                                                                                                                                                                                                                                                                                                                                                 carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3
                                                                                                                                           Disclosure; Page 83-85; 94pp; English.
                                               Dalton W;
38-SEP-2000; 2000US-0231212P
                                               Pardoll D, Jove R,
                                                                                             Modulating angiogenesis and
                 (UYSF-) UNIV JOHNS HOPKINS.
                                                                WPI; 2002-362218/39.
                                                                                                                         of transcription 3.
                                                                          N-PSDB; AAD35065
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compound th
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AAE22056 standard; protein; 769 AA. 25-JUL-2002 (first entry) AAE22056; AAE22056 RESULT SAXAXEX

immuni response; Stati; coronary atterosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoxlycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative diseorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative diseorder; lesion. signal transducer and activator of transcription 3; ischaemia Human protein related to angiogenesis regulation. 

WO200220032-A1 Homo sapiens.

14-MAR-2002.

10-SEP-2001; 2001WO-US028254.

08-SEP-2000; 2000US-0231212P. (UYJO ) UNIV JOHNS HOPKINS. (UYSF-) UNIV SOUTH FLORIDA.

Dalton W; Yu H, Pardoll D, Jove R,

WPI; 2002-362218/39.

Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator of transcription 3.

Disclosure; Page 83-85; 94pp; English.

coclusion, prenatal or postnatal coxygen deprivation, transmin, vasculation constructive pulmonary disease, choking, asphyxia, hypoglycaemia, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, capilepsy, emphysema, adult respiratory distress syndrome, carrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, slogren's syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious maemia, autoimmune thyroiditis, didopathic Addison's disease, vitiligo, gluten sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, disease, theumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and disease. The method is useful in preventing or treating carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leuksemia, myasthenia, myasthenia gravis, humbored it infertility and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leuksemia, myasthenia, myasthenia, myasthenia, myasthenia, myasthenia, myasthenia, proventing or treating carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leuksemia, myasthenia, myasthe The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, asscular physical trauma, lesions and wounds. I herapy. The present sequence is human method is also used in gene therapy. The pi protein related to angiogenesis regulation disorders, hypoproliferative

Sequence 769 AA;

Gaps ; 0 Query Match 100.0%; Score 669; DB 5; Length 769; Best Local Similarity 100.0%; Pred. No. 4.6e-68; Matches 129; Conservative 0; Mismatches 0; Indels 0

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249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
                                                                                                                                                                                                                                                                                                                          29-MAR-1995;
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                                                                                                                                                                                                                                                                Signal transducer and activator of transcription; STAT; 198f6; Stat3; receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                            1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
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100.0%; Score 669; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0;
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                                                                                                                                                                         AAR72082 standard; protein; 770 AA.
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93US-00126595.
94US-00212184.
94US-00212185.
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(first entry)
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                                                                                                    DKDSGDVAA 129
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N-PSDB; AAQ89340.
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11-MAR-1994;
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27-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
Mouse; acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as \mathrm{IL}^-6, e.g. inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse liver acute phase response factor.
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                                                                                                                                                                                                                                                                               AAR82995 standard; protein; 770 AA
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g. oncogenesis, inflammation, parasitic disease or autoimmunity.
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100.0%; Pred. No. 4.6e-68;
iive 0; Mismatches 0;
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/label= DNA_binding_domain
/note= "Claim 3, page 110"
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                                                                AAW03176 standard; protein; 770 AA.
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Matches 129; Conservative
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121 DKDSGDVAA 129
                                                                                                                                                                                                                                                                                                                                                                                                  Wen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-333941/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT31280.
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                                                                                                                                                                                                                                                                                                                               28-DEC-1995;
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                                                                                                               24-OCT-1996
                                                                                                                                                                                                                                                                                                         11-JUL-1996.
                                                                                                                                     Mouse STAT4
                                                                                                                                                                                                                                                                                                                                                                                                  Darnell JE,
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                                                                                       AAW03176;
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                                                                                                                                                                                                                                                        Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
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100.0%; Pred. No. 4.6e-68;
ive 0; Mismatches 0;
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'AAY03768 standard; protein; 770 AA.
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                                                                                                                                                                                               Human STAT3 allelic variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-192664/17.
N-PSDB; AAX29281.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.
                                                                                                                                         STAT; signal transducer and activator of transcription; crystal;
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                                                                                                                                                                                                                                                                                                                                                                                                          alpha helix
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                                                                                              N-terminal domain of murine STAT-3 protein.
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/label= 3(10) helix of
28. .33
/label= Alpha helix 3
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/label= Alpha helix 1
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Matches 129; Conservative
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                                                                                                                                                                       drug design; murine.
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                                               08-NOV-2000
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AAB12377;
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The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that binds to the N-terminal domain of a STAT protein, compound that enhances or diminishes the binding of the identifying a compound that enhances or diminishes the ability of site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new drugs. An antagonist of STAT N-terminal dimeric interactions that control of a gene operably under containing at the treatment of a promoter of a gene, could be useful as drugs in the treatment of diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other can be used as drugs in the treatment of diseases e.g. anaemia, can be used as drugs in the treatment of diseases e.g. anaemia, contropaemia, thrombocytopaemia, cancer, obesity, viral diseases and content by the present sequence is murine STAT3 protein
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                                                                                                                                                                                                                                                                                                                                             Signal transducer and activator of transcription; STAT3; drug development; drug discovery; crystal; inflammation; allergy; asthma; leukaemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity; viral disease; growth retardation; murine.
309 IVELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying compounds that bind to signal transducer transcription proteins, useful for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuriyan J;
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                                                                                                   369 pkpscpvaa 377
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1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER

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(forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polymucleotides in adipocyte encoding for the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for the recombinant host cell which is transformed with two vectors, where the first vector comprises a polymucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polymucleotide encoding a second vertor comprising a polymucleotide encoding a second reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the recombinant host cell (i.e. using the yeast two-hybrid system). The
                249 IACIGGPPNICLDRLENWITSLAESQLOTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
                                                                                                  Human, yeast two-hybrid assay, adipocyte, bait protein, NIDDM,
non-insulin diabetes mellitus, obesity, selected interacting domain, SID,
protein-protein interaction map, PIM, anorectic, metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complexes are useful for identifying compounds that modulate the protein-
protein interactions and useful for treating obesity and metabolic
disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The
compound isolated by the method is useful for treating and preventing
obesity or metabolic diseases. The interactions between the proteins of
the complex further define a set of selected interacting domains, SID.
                                                                           61 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders.
1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a complex of protein-protein interactions
                                                                                                                                                                                                                                                                                                   ABG69497 standard; protein; 770 AA.
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(CNRS ) CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human bait protein STAT3.
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The present sequence represents a member of the protein complex of the invention, used as the bait protein in the yeast two- hybrid assay
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                                                                                        Length 770;
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Job time : 70.83 secs
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                                                                                                                                     1 IACIGGPPNICLDRLENWIT......LNYQLKIKVCIDKDSGDVAA 129
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-387-418A-23
US-09-387-418A-22
US-09-387-418A-9
US-08-16-581B-9
US-08-16-581B-9
US-08-16-581B-9
US-08-12-09-12
US-08-956-652-12
US-08-956-869-12
US-09-364-970-3
US-09-364-970-3
US-09-364-970-3
US-09-364-970-5
US-09-364-970-5
US-09-556-653-12
US-09-556-653A-12
US-09-556-653A-12
US-09-556-653A-12
US-09-556-653A-12
US-08-526-542-2
US-08-117-087-2
US-08-117-087-2
US-08-117-087-2
US-08-117-581B-1
US-08-416-581B-1
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US-09-387-418A-18
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                                                                                                                                                                                            513545 seqs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 24, Application US/09387418A
| GENERAL INFORMATION: Macasaczynska, Melissa H
| APPLICANT: Morvath, Curr M
| APPLICANT: Morvath, Curr M
| APPLICANT: Darnell Jr., James E
| TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR |
| TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR |
| FILE REFERENCE: 600-1-253 |
| CURRENT APPLICATION NUMBER: US/09/387,418A |
| CURRENT FILING DATE: 1999-08-31 |
| NUMBER OF SEQ ID NOS: 43 |
| SOFTWARE: PatentIn Ver. 2.0
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; Sequence 23, Application US/09387418A
; Sequence 23, Application US/09387418A
; Patent No. 6341572
; GENERAL INFORMATION:
; APPLICANT: Chang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvach, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
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US-09-387-418A-28

US-09-387-418A-31

US-09-387-418A-31

US-09-387-418A-29

US-09-387-418A-29

US-09-387-418A-19

US-09-387-418A-19

US-09-387-418A-19

US-09-387-418A-19

US-09-387-418A-19

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US-09-387-418A-19

US-09-387-418A-12

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US-09-387-418A-12

US-09-387-418A-12

US-08-36-754-6

US-08-956-655-6

US-08-956-655-6

US-08-956-653-6

US-08-956-653-6

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     DKDSGDVAA 129
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ORGANISM: Mus musculus
     US-09-387-418A-24
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LENGTH: 129
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APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT APPLICATION NUMBER: US/09/387,418A
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VOY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Chorg Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mander & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                             143 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 202
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                   100.0%; Score 669; DB 3;
100.0%; Pred. No. 1.5e-68;
tive 0; Mismatches 0;
Wrzeszczynska, Melissa H
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; Patent No. 5716622
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CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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IELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 129; Conservative
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US-09-387-418A-9
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                                                                                                                                                                                                                                 Query Match 100.0%; Score 669; DB 3; Length 185; Best Local Similarity 100.0%; Pred. No. 8.9e-69; Matches 129; Conservative 0; Mismatches 0; Indels
             CURRENT APPLICATION NUMBER: US/09/387,418A CURRENT FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 43 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/387,418A CURRENT FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 43 SOFTWARE: Patentin Ver. 2.0
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Patent No. 6391572
PERERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.(
Matches 129; Conservative
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CORGANISM: Mus musculus
US-09-387-418A-22
                                                                                                                                                 TYPE: PRT ORGANISM: Mus musculus
    FILE REFERENCE:
                                                                                                                                                                                            US-09-387-418A-23
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US-09-387-418A-9
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APPLICANT: Jang Wen
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Curt M. Horvath
APPLICANT: Chong Zhong Zho
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309 IVELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYGLKIKVCI 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08852091
Patent No. 5883228
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CITY: Hackensack
STATE: New Jersey
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 343-1684
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                                                                                                   DKDSGDVAA 129
                                                                                                                                                               369 pkösgövák 377
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                                                                                                                                                                                                                                                                                           US-08-852-091-12
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                                                                                                                                 DB 1; Length 770;
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APPLICATION NUMBER: US/08/416,5415 CLASSIETATO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
                                                                                                                           100.0%; Score 669; DB 1
100.0%; Pred. No. 6e-68;
iive 0; Mismatches
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100.0%; Pred. No. 6e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/416,581B FILING DATE: 04-APR-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 6-65825/1994 FILING DATE: 04-APR-1994 ATORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08416581B Patent No. 5719042
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REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: 0-7
TELECOMMUNICATION INFORMATION:
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amino acid
                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 129; Conservative
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Best Local Similarity 100.
Matches 129; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TOPOLOGY: linear MOLECULE TYPE: protein
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                                                               US-08-369-796-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-416-581B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-416-581B-9
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249 IACIGGPPNICLDRLENWITSLABSQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
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                                                                              Sequence 12, Application US/08956652
Patent No. 6013475
GENERAL INFORMATION:
PAPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: W. Xian-Yuan
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCES ADDRESSEE: Klauber & Jackson
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 669; DB 3; Length 770; 100.0%; Pred. No. 6e-68; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS'
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
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REGISTRATION NUMBER: 26,742
REFERENCE JOCKET NUMBER: 600-1-073 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-MOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 24-SEP-1993
ATTORNEY AGENT: 18-PAR-1993
ATTORNEY AGENT: NFORMATION:
NAME: 13-MAR-1093
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INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISICS: LENGTH: 770 amino acids
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amino acid
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Best Local Similarity 100.
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                             -08-956-652-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
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Sequence 12, Application US/08820754
Fatent No. 5976835
GENERAL INPOMATION:
APPLICANT: Darnell Jr., James B.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Tolong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                       ADDRESESE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1997
RILING DATE: 13-MAR-1997
APPLICATION NUMBER: US 07/980,498
FILING DATE: 13-MOV-1992
RICK APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
RICK APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
RICK APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
RICK APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
RICK APPLICATION NUMBER: US 08/126,588
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 129; Conservative
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249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING STATEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILLING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          3: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                        APPLICANT: Vinkemeier, Uwe APPLICANT: Moarefi, Ismail APPLICANT: Moarefi, Ismail APPLICANT: Darnell, Jr., James E. APPLICANT: Kuriyan, John TITLE OF INVENTION: A CRYSTAL OF THE N-TITLE OF INVENTION: STAT PROTEIN AND ME NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-948-547-12
'Sequence 12, Application US/08948547
'Patent No. 6124118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
                                                                                                                                                                          Sequence 8; Application US/09012710 Patent No. 6087478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Hackensack
STATE: New Jersey
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ZIP: 07601
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                                                                                                                                                                                                          APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/956,869
                                                                                                                                                   Sequence 12, Application US/08956869
Patent No. 6030808
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,185
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                       Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Bsg., David A. REGISTRATION NUMBER: 26,742
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.0
Matches 129; Conservative
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MEDIUM TYPE: Floppy
                         369 DKDSGDVAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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DKDSGDVAA 129
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                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Mus musculus
US-09-364-970-3
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                                                                                                                                                                                                                                                                                  SEQ ID NO 3
LENGTH: 770
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APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,547
FILING DATE: 11-MAR.1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 13-NOV 1992
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV 1992
APPLICATION NUMBER: US 07/980,498
FILING DATE: 19-MAR.1994
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR.1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 19-MAR.1993
APPLICATION NUMBER: GOD-1-073 CIP
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELEPHONE: 201 487-5800
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100.0%; Pred. No. 6e-68;
tive 0; Mismatches
                                                                                                                                                                          STREET: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA ZIP: 07601
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Matches 129; Conservative
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US-08-948-547-12
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RESULT 13

249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308 308 309 IVELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368 61 IVELFRNIAMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120 309 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368 Sequence 3, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: USER PROJEFRATIVE CELLULAR CHANGES
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VEY: 2.0 US-09-364-970-5

Sequence 5, Application US/09364970

Sequence 5, Application US/09364970

Sequence 5, Application US/09364970

Sequence 5, Application US/09364970

GENERAL INFORMATION:

APPLICANT: Bromberg, Jacqueline

TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING

TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING

FILE REFERENCE: 600-1-252

CURRENT APPLICATION NUMBER: US/09/364,970

CURRENT FILING DATE: 199-07-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PATENTIN Ver. 2.0 249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER IVELPRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER Gaps . 0 DB 3; Length 770; Query Match 100.0%; Score 669; DB 3; Length 770; Best Local Similarity 100.0%; Pred. No. 6e-68; Matches 129; Conservative 0; Mismatches 0; Indels 0 Query Match
100.0%; Score 669; DB 3; Length 77
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels

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249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 IVELFRNIAMKSAFVVERQPCMFWHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 60
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DB 3; Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 669; DB 3; Length 7
100.0%; Pred. No. 6e-68;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                STATE: New Jersey
COUNTRY: USA
ZIP: 07601

ZIP: 07601

COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATOMIL RElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,273
                                                                                                                                                                                                                               E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson EQ, David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECHONE: 201-487-5800
TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFCATION:
PRICH APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 129; Conservative
                                                                                                                                                                                        NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & J
STREET: 411 Hackensack
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO US-09-556-273-8
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369 DKDSGDVAA 377
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Search completed: May 25, 2005, 17:47:38 Job time : 17.141 secs THIS PAGE BLANK (USPTO)

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US-10-090-185-24
; Sequence 24, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
paper Applicant Warden Malisea
                                                                                                                                                                             May 25, 2005, 17:36:58 ; Search time 56.4935 Seconds (without alignments) 763.830 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                               1 IACIGGPPNICLDRLENWIT.....LNYQLKIKVCIDKDSGDVAA 129
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1434725 seqs, 334507595 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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669
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115:
117:
119:
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                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                      Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 24, Appl	Sequence 23, Appl	Sequence 22, Appl	6	Sequence 4, Appli	7	Sequence 5, Appli	12,	8		Sequence 2, Appli	Sequence 12, Appl	Sequence 780, App
	TD	US-10-090-185-24	US-10-090-185-23	US-10-090-185-22	US-10-090-185-9	US-10-380-020-4	US-10-380-020-2	US-10-380-020-5	US-09-876-773-12	US-10-045-792-8	US-10-038-010-56	US-10-117-087-2	US-10-639-617-12	US-09-925-302-780
	DB	13	13	13	13	15	15	15	11	14	14	14	17	6
	Query Match Length DB ID	129	185	223	271	720	769	769	770	770	770	770	770	793
ф	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	699	699	699	699	699	699	699	699	699	699	699	699	699
	Result No.	7	7	٣	4	2	9	7	80	σ	10	11	12	13

Sequence 780, App Sequence 319, App Sequence 349, App Sequence 18, Appl Sequence 21, Appl Sequence 21, Appl Sequence 25, Appl Sequence 12, Appl Sequence 12, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 32, Appl Sequence 32, Appl Sequence 4, Appl Sequence 352, Appl Sequence 250, Appl Sequence 550, Appl	a a a
10 US-09-925-302-780 15 US-10-116-275-349 13 US-10-090-185-18 13 US-10-090-185-28 13 US-10-090-185-28 13 US-10-090-185-31 13 US-10-090-185-14 13 US-10-090-185-14 13 US-10-090-185-19 13 US-10-090-185-19 13 US-10-090-185-19 13 US-10-090-185-19 14 US-10-090-185-15 15 US-09-876-713-6 17 US-10-639-617-6 18 US-10-638-617-6 18 US-10-638-617-6 19 US-09-876-773-4 14 US-10-638-617-6 16 US-10-936-898-823 17 US-10-755-889-823 18 US-10-755-889-823 18 US-10-755-889-955 19 US-09-935-550 11 US-10-639-617-4 10 US-10-755-889-955 11 US-10-755-889-955 12 US-09-935-550 13 US-09-935-550	9 US-09-833-205-4 11 US-09-833-205-6 14 US-10-045-792-7 14 US-10-205-194-39
793 770 770 770 770 770 722 722 723 723 723 711 7112 7112 7112	4477 4444 60000
666 9 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
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## ALIGNMENTS

IVATOR			
ACT	, 0	09	20
TRANSCRIPTIONAL	Length 129; Indels 0; Gaps	SDPIVQHRPMLEER 6	PELNYQLKIKVCI 1:
о О	Length	JSYKC 	T AKE
APPLICANT: Wrzeszczynska, Melissa H APPLICANT: Horvath, Curt M APPLICANT: Darnell Jr., James E APPLICANT: Darnell Jr., James E ATTILE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR TITLE OF INVENTION: INTERACTIONS TITLE OF INVENTION: INTERACTIONS TITLE OF INVENTION: MUMBER: US/10/090,185 CURRENT APPLICATION NUMBER: 09/387,418 PRIOR PELING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 43 SOFTWARE: PATENTI Ver. 2.0 EQ ID NO 24 LENGTH: 129 TYPE: PATENTI OF THE OFFICE	100.0%; Score 669; DB 13; 100.0%; Pred. No. 9.6e-67; ative 0; Mismatches 0;	1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER	61 IVELFRNIAKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLVKFPELNYOLKIKVCI 120 
APPLICANT: Wrzeszczynska, Me APPLICANT: Horvath, Curt M APPLICANT: Darnell Jr., Jame TITLE OF INVENTION: METHODS F TITLE OF INVENTION: INTERACT TITLE OF INVENTION: INTERACT TITLE OF INVENTION: METHODS F TITLE OF INVENTION: INTERACT PRIOR EPPLICATION NUMBER: 09 PRIOR APPLICATION NUMBER: 09 PRIOR APPLICATION NUMBER: 09 PRIOR PELICATION NUMBER: 09 PRIOR PELICATION NUMBER: 09 PRIOR APPLICATION NUMBER: 09 PRIOR APPLICATION NUMBER: 09 PRIOR APPLICATION NUMBER: 09 PRIOR APPLICATION NUMBER: 09 TOWN APPLICATION NUMBER: 09 TOWN APPLICATION NUMBER: 09 TOWN APPLICATION NUMBER: 09 TOWN APPLICANT NUMBER: 09 TOWN APPLICATION NUMBER: 09 TOWN APPLICAT	Query Match Best Local Similarity 100. Matches 129; Conservative	1 IACIG	61 IVELFI         OELFI
us.		8 8	8 8

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Sequence 4, Application US/10380020
; Sequence 4, Application US/10380020
; Publication No. US2004005276A1
; GENERAL INFORMATION:
    APPLICANT: Vu, Hua
; APPLICANT: Daton, Willian
; TITLE OF INVENTION Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT PLING DATE: 2003-03-07
; PRIOR PPLICATION NUMBER: 60/231,212
; PRIOR PPLICATION NUMBER: 60/231,212
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Version 3.0
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 262
                                                                                                        61 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPBLNYQLKIKVCI 120
                                                 95 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                 1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
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                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/10090185; Sequence 9, Application US/10090185; Publication No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Macsezczynska, Melissa H
APPLICANT: Aparg, Xiaokui
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
TITLE OF INVENTION: METHODS FOR IDENTIFYING;
TITLE OF INVENTION: METHODS FOR IDENTIFYING;
TITLE OF INVENTION: MUMBER: US/10/090,185
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 09/387,418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 271
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                                                                                                                                                                                                                                                         215 DKDSGDVAA 223
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, ORGANISM: Mus musculus
US-10-090-185-9
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                                                                                                                            US-10-090-185-23

Sequence 23, Application US/10090185

Publication No. US2020197647A1

GENERAL INFORMATION:

APPLICANT: Anang, Xiaokui

APPLICANT: Arzeszczynska, Melissa H

APPLICANT: Borreath, Curt M

APPLICANT: Borreath, Curt M

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-1-253

CURRENT FILING DATE: 2002-03-04

PRIOR PLICATION NUMBER: 09/387,418

PRIOR PLICATION DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOUTHMER: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/10090185
Sequence 22, Application US/10090185
Sequence 22, Application No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Stansy, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT PAPLICATION NUMBER: 09/387,418
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR PILING DATE: 1999-08-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI
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100.0%; Pred. No. 1.9e-66;
iive 0; Mismatches 0;
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100.0%; Score 669; DB 13;
Best Local Similarity 100.0%; Pred. No. 1.5e-66;
Matches 129; Conservative 0; Mismatches 0;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 223
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Best Local Similarity 100.
Matches 129; Conservative
                                            DKDSGDVAA 129
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CRGANISM: Mus musculus
US-10-090-185-23
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Length 769; Indels

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249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
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Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
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                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 669; DB 15; Best Local Similarity 100.0%; Pred. No. 9.6e-66; Matches 129; Conservative 0; Mismatches 0;
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NAME: Jackson Eng., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
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FILING DATE: 19-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-JUN-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
  CURRENT APPLICATION NUMBER: US/10/380,020 CURRENT FILING DATE: 2003-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09876773
; Publication No. US20040058318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E. Schindler, Christian W.;
                          CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION WUNBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
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                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5
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APPLICANT: Pardoll, Drew
APPLICANT: Dato, Richard
APPLICANT: Jove, Richard
APPLICANT: Journal Millian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: 60/231,212
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
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APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
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8.8e-66;
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100.0%; Pred. No. 9.6e-66;
tive 0; Mismatches 0;
                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 8.8
Matches 129; Conservative 0; Mismatches
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Publication No. US20040052762A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10380020 Publication No. US20040052762A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 129; Conservative
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                                          , ORGANISM: Homo Sapiens
US-10-380-020-4
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LENGTH: 720
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61 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/10038010
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
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                                                                                                                                                       Length 770;
                                                                                                                                                     Query Match
100.0%; Score 669; DB 14;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0;
                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8
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Publication No. US20030166854A1
GENERAL INFORMATION:
APPLICANT: SERLUPI-CRESCENZI, Ottaviano
APPLICANT: DELLA PIETRA, Linda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: STAT3 : Transcription factor
; LOCATION: (1) .. (770)
; OTHER INFORMATION:
US-10-038-010-56
STRANDEDNESS: single
                     TOPOLOGY: linear MOLECULE TYPE: protein
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Best Local Similarity 100.
Matches 129; Conservative
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ORGANISM: Homo sapiens
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US-10-038-010-56
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US-10-117-087-2
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Moarefi, Ismail
Darnell, Jr., James E.
Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                   Length 770;
                                                                                                                                                                                                                                                                                                                                              Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 669; DB 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10045792 Publication No. US20030003563A1 GENERAL INFORMATION:
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                                                           TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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                          TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKDSGDVAA 129
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Gaps

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61 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
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JOHNERAL INFORMATION: Nucleic Acids, Proteins and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REPERENCE:

CURRENT APPLICATION NUMBER: US/09/925,302

FRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR PELLING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03.12

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 669; DB 9; Length 793; 100.0%; Pred. No. 1e-65; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 669; DB 17;
100.0%; Pred. No. 9.6e-66;
Live 0; Mismatches 0;
                                      : 600-1-073 CIP
                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
             REGISTRATION NUMBER: 26,742
                                    REFERENCE/DOCKET NUMBER: (TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-925-302-780
; Sequence 780, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
                                                                             TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                      Matches 129; Conservative
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Best Local Similarity 100.
Matches 129; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                Similarity
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US-09-925-302-780
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TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                     Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/639,617

FILING DATE: 12-Aug-2003

CLASSIFICATION: 435

FRIOR APPLICATION ATA:

APPLICATION NUMBER: US/08/212,185

FILING DATE: 11-Aug-1994

APPLICATION NUMBER: US 07/980,498

FILING DATE: 23-NOV-1992

APPLICATION NUMBER: US 07/854,296

FILING DATE: 19-MAR-1993

APPLICATION NUMBER: WO US93/02569

FILING DATE: 19-MAR-1993

APPLICATION NUMBER: WO US93/02569
                                                                                                                                                                                                                                                                                                                                                                Indels
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3;
FILE REFERENCE: SERLUPI=2;
CURRENT APPLICATION NUMBER: US/10/117,087
CURRENT FILING DATE: 2002-04-08;
PRIOR APPLICATION NUMBER: US/09/526,542;
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2:
LENGTH: 770
                                                                                                                                                                                                                                                                                                                  100.0%; Score 669; DB 14; 100.0%; Pred. No. 9.6e-66;
                                                                                                                                                                                                                                                                                                                                                             Mismatches
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US-10-639-617-12
Sequence 12, Application US/10639617
Publication No. US20050079543A1
GENERAL INFORMATION:
Schindler, Christian W.
Fu. Xian-Yuan
Wen, Zilong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
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Best Local Similarity 100.
Matches 129; Conservative
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; ORGANISM: Human
US-10-117-087-2
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Search completed: May 25, 2005, 18:21:51 Job time : 59.8269 secs
    121 DKDSGDVAA 129
                                             369 pkpsgpvAA 377
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APPLICANT: Byrne, Daragh
APPLICANT: Byrne, Daragh
APPLICANT: Lambkin, Imedia
APPLICANT: Lambkin, Imedia
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REPERBUCE: B1067/20087
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEC ID NOS: 349
SOFTWARE: PatentIn version 3.1
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100.0%; Score 669; DB 10; Length 793;
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 129; Conservative 0; Mismatches 0; Indels 0
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Pred. No. 2.1e-65;
1; Mismatches 0; Indels 0
                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAIO4 WINDER: US/09/925,302
CURRENT APPLICATION NUMBER: US/09/925,302
PRICR APPLICATION NUMBER: PCT/US00/05918
PRICR PLING DATE: 2000-03-08
PRICR FILING DATE: 1099-03-08
PRICR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 342). ... US2003v2....
Publication No. US2003v2....
GENERAL INFORMATION:
APPLICANT: Blan Pharmaceutical Technology
APPLICANT: O'Mahony, Daniel J.
Sequence 780, Application US/09925302
Publication No. US20030064072A9
GENERAL INFORMATION:
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Best Local Similarity 99.2
Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-302-780
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; ORGANISM: Rat
US-10-116-275-329
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LENGTH: 770
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OM protein - protein search, using sw model

Run on:

May 25, 2005, 17:24:07 ; Search time 12.1698 Seconds
(without alignments)
1019.898 Million cell updates/sec

1 IACIGGPPNICLDRLENWIT......LUNYQLKIKVCIDKDSGDVAA 129 US-10-090-185-24 699 Perfect score: Sequence:

**BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	, Length	DB	QI	Description
٦	699	100.0	770	2	149508	ISGF3 p91-related
7	664		1770	~	A54444	DNA-binding protei
٣	390.5	28		7	A46159	interferon-depende
4	375	Ŋ			A56047	gamma-interferon a
Ŋ	257	38.4	851		A46160	interferon alpha-i
9	160.5	N			I49274	mammary gland fact
7	160.5	24.0			S54772	qland
œ	160.5	24.0	79	~	G02317	
σ	142	21.2	79	7	855527	mammary gland fact
10	86	14.6			A54740	
11	•	14.0			157557	DNA-Binding Protei
12	80.5	12.0			H90279	
13	80	12.0			T25063	hypothetical prote
14	79	11.8			NDECAS	type I site-specif
15	78.5	11.7			B70042	hypothetical prote
16	78.5	11.7			F84840	hypothetical prote
17	78	11.7			T06667	argininosuccinate
18	77	11.5			A48461	ovarian abundant m
19	75.5	11.3			B96003	probable transcrip
20	75.5	11.3	926		T39082	hypothetical prote
21	75	11.2			G90550	
22	75	11.2			G81420	hypothetical prote
23	75	11.2			T39954	probable otpase ac
24	74.5	11.1			T48076	60S RIBOSOMAL PROT
25	74.5	11.1			T14277	myosin-like protei
56	74.5	11.1			A41948	alpha-fetoprotein
27	74	11.1	. 893	~	F72253	hypothetical prote
28	73	10.9		~	AC2368	
58	73	10.9	575	0	AF2374	

ribosomal protein	hypothetical prote	HST3 protein - yea	golgin-245 - mouse	xanthine dehydrode	hypothetical prote	protein T22C1.6 [i	4-hydroxyphenylpyr	4-hydroxyphenylpyr	myosin heavy chain	heat shock protein	conserved hypothet	hypothetical prote	probable protein k	unconventional myo	breast cancer susc
T00423	A85040	S54631	T14265	XORTDH	T25110	F87844	S32458	832821	S21801	873360	A99345	A86253	F96558	A59310	T42205
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257	432	447	1218	1331	335	346	393	393	1999	217	328	573	879	1529	3329
10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.7	10.7	10.7
72.5	72.5	72.5	72.5	72.5	72	72	72	72	72	71.5	71.5	71.5	71.5	71.5	71.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

C;Species: Mus musculus (house mouse)
C;Date: 02-01-1996 #sequence\_revision 02-011-1996 #text\_change 09-Jul-2004
C;Date: 02-01-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004
C;Accession: 149509; 149509; 149009; X.J.; Waig, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRP, a novel IFN-stimulated gene factor 3 p91-related tr
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: 149508
A;Accession: I49508
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-770 <RES> A;Cross-references: UNIPROT:P42227; GB:L29278; NID:g476715; PIDN:AAA37254.1; PID:g47671 R;Raz, R.; Durbin, J.E.; Levy, D.E. D Biol. Chem. 269, 24391-24395, 1994 A;Title: Acute phase response factor and additional members of the interferon-stimulate A;Reference number: 149009; MUID:95014185; PMID:7523373 ö 249 IACIGGPPNICLDRLENWITSLAESQLOTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308 61 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPBLNYQLKIKVCI 120 309 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368 9 A;Residues: 1-393,'M',395-700,702-770 <RE2> A;Cross-references: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890 C;Genetics: 1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER Gaps A;Gene: APRF C;Superfamily: human signal transducer and transcription activator STATSA ö Length 770; Query Match 100.0%; Score 669; DB 2; Length 7 Best Local Similarity 100.0%; Pred. No. 1.8e-55; Matches 129; Conservative 0; Mismatches 0; Indels A;Accession: 149009 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA p91-related transcription factor - mouse DKDSGDVAA 129 121 g 셤 ઠે ò ò

369 DKDSGDVAA 377 셤

RESULT 2 A54444 DNA-101ding protein APRF - human C;Species: Homo sapiens (man) C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004 C;Datesion: A5444 R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su

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A;Molecule type: DNA
A;Residues: 1-851 <YAN>
                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                       A; Residues: 1-748 < YAM>
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                                                                                                                                                    A; Molecule type: mRNA
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A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG A;Reference number: A46159; MUID:92366557; PMID:1502203
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Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related
A;Reference number: A54444; MUID:94208062; PMID:7512451
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Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELHQKVSYKGDPIVQHRPMLEER
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                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Rosidues: 1-770 cRES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
C;Genetics:
A;Gene: GDB:STAT3; APRF
A;Cross-references: GBB:358950
A;Map position: 17q21-17q21
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor
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C;Superfamily: human signal transducer and transcription activator STAT5A
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                                                                                                                                                                                                                                                                                                                         99.3%; Score 664; DB 2;
99.2%; Pred. No. 5.5e-55;
iive 0; Mismatches 1;
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Matches 128; Conservative
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Best Local Similarity
---- 74; Conserve
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                                                                A; Accession: A54444
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gamma-interferon activation site-binding protein Stat4 - mouse C,Species: Mus musculus (house mouse) C,Species: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004

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C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, Mol. Cell. Biol. 14, 4342-4349, 1994
Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status; preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P42228; GB:U09351; NID:G509502; PIDN:AAA19692.1; PID:G50950 C;Superfamily: human signal transducer and transcription activator STAT5A C;Keywords: DNA binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Fu, X.Y.; Schindler, C.; Improta, T.; Aebersold, R.; Darnell Jr., J.E. Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
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R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in A;Reference number: S53873; MUID:95192056; PMID:7885841
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C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
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Pred. No. 1.3e-27;
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A;Residues: 1-196;392-591;684-730 <YAW>
A;Cross-references: EMBL:U18671
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59.3%;
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Matches 5
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A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:Z48538; NID:g758633; PIDN:CAA8 R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L. Proc. Natl. Acad. Sci. US.A. 92, 8831-8835, 1995 A;Title: Cloning and expression of Stats and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
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C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regul
A;Reference number: 855527; MUID:95188889; PMID:7882987
A;Rocession: 855527
A;Molecule type: mRNA
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A,Residues: 1-794 <LIN>
A,Cross-references: UNIPROT:P42229; EWBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g11
C,Superfamily: human signal transducer and transcription activator STATSA
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C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 24.0%; Score 160.5; DB 2; Length 793; 1 Similarity 37.6%; Pred. No. 3e-07; 38; Conservative 17; Mismatches 37; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 794;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 FRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLV 105
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A;Reference number: S54772; MUID:95237198; PMID:7720707 A;Accession: S54772
A;Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                           A;Accession: 149273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Conservative
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                                                                                            A; Molecule type: mRNA
A; Residues: 1-793 <MUI>
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MyAlternate names: stat5 protein
MyAlternate names: stat5 protein
C;Species 100
C;Decies 100
C;Date: 27-Oct-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54772; I49273
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
BMB0 0. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:P42232; UNIPROT:09JKM1; EMBL:U21110; NID:g747973; PIDN:AAC52 RK;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A. EMBO J. 1175, 1995
EMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin A;Reference number: S54772; MUID:95237198; PMID:7720707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 17432, E', 434-786 <MUI>
A;Cross-references: EMBL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R;Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris, EMBO J. 14, 1402-1411, 1995
A;Title: Interleukin-3 signals through multiple isoforms of Stat5.
A;Reference number: S54725; MUID:95246733; PMID:7537213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NiAlternate names: STATS protein homolog p80
Cispecies: Mus musculus (house mouse)
Cjate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
CjAccession: 149274; S54773; S54727
Rilu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Rilu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
A;Title: Cloning and expression of Stats and an additional homologue (Statsb) involved
A;Reference number: 149273; MUID:96004632; PMID:7568026
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                                                                                                                                                            30S TELLQRILHRAFVVETQPCMPQTPHRPLILKTGSKFTVRTRLLVRLQEGNESLIVEVSID 364
                                   265 GGPPEGSLDVLQSWCEKLAEIIWONROOIRRAEHLCOOLPIPG-PVEEMLAEVNATÍTDI 323
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      61
ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                         62 VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCID
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-432,'E',434-786 <AZA>
A;Genetics:
A;Genetics:
C;Superfamily: human signal transducer and transcription activator STATSA
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A, Status: preliminary; nucleic acid sequence not shown
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-786 <RES>
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les 38; Conserv
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RN 366
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Best Local S
Matches 38
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A; Gene: SS01256
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C;Genetics:
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C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 157557
R;Quelle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Cleve Mol. Cell. Biol. 15, 3336-3343, 1995
A;Title: Cloning of murine Stat6 and human Stat6, Stat proteins that are tyrosine phosph A;Reference number: 157557; MUID:9528094; PMID:7760829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-837 <RES>
A;Cross-references: UNIPROT:P52633; GB:L47650; NID:g1008876; PIDN:AAA79006.1; PID:g10088
                      A;Cross-references: UNIPROT: P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g6023 A;Note: this is a revision to the sequence from reference S44353 B;Note: this is a revision to the sequence from reference S44353 B;Note: this is a revision to the sequence from reference S44353 A;Note: this is a revision to the sequence from reference S44353; MUID:94244619; PMID:7514531 A;Reference number: S44353; MUID:94244619; PMID:7514531 A;Residues: 1-716, RH:HIGPGSLPSR', 729, 'P', 731, 'ASL' <WAW> A;Residues: 1-716, RH:HIGPGSLPSR', 729, 'P', 731, 'ASL' <WAW> Cross-references: EMBL:X78428 A;Note: this sequence has been revised in reference S55527 C;Superfamily: human signal transducer and transcription activator STAT5A
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A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
A;Accession: A54740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Homo sapiens (man)
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A,Molecule type: mRNA
A,Residues: 1-848 <HOUD-
A,Cross-references: UNIPROT: P42226
C,Superfamily: human signal transducer and transcription activator STATSA
C,Keywords: DNA binding; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: | |::|:|| 356 ALVTSTFIIEKQP------PQVLKTQTKFAATVRLLV 356
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microtubule binding protein, probable [imported] - Sulfolobus solfataricus C; Species: O: Sungh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffrias, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: UNIPROT: Q9UXN4; GB: AE006641; NID: g13814451; PIDN: AAK41495.1; GSPDB: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q22633; EMBL:Z50016; PIDN:CAA90315.1; GSPDB:GN00021; CESP:T|
A;Experimental source: clone T21C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                               214 GTPFEESLAGLQERCESLVEIYSQLHQEIGAASGELEPKT------RASLISRLDE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
C;Accession: T25063
                                                                                                                                                                                                                       5 GGPPNICLDRLENWITSLAESQLQTRQQIKKLE-ELQQKVSYKGDPIVQHRPMLEERIVE
A;Gene: STAT6
C;Superfamily: human signal transducer and transcription activator STAT5A
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                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                  64 LFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLV 105
                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein T21C12.2 - Caenorhabditis elegans
                                                                                      ch 14.0%; Score 93.5; DB 2; Similarity 32.4%; Pred. No. 0.71; 33; Conservative 12; Mismatches 38;
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submitted to the EMBL Data Library, July 1995
A;Reference number: Z19976
A;Accession: T25063
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393 <WILL>
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                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <KUR>
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R;Cowan, G.M.; Gann, A.A.F.; Murray, N.E.
Cell 56, 103-109, 1989
A;Title: Conservation of complex DNA recognition domains between families of restriction A;Reference number: A32343; MUD:89089749; PMID:2642743
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Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997
Cipate: Cipate
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C.Superfamily: type I site-specific deoxyribonuclease EcoA chain S
C.Keywords: DNA binding; hydrolase; restriction modification system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 CVGNOPDLOMDSAVOWYEKVLKFHRFWSVDDSMIHTEYSALRSIVVTNFEETIKMPINEP 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 ATSDKKAISQIQEYVDYYGGSGVQHIALNTSDIITALEALRARGCEFLSIPSSYYDNLKE 302
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23; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CIGGPPNICLDRLENW------ITSLAESQLQTRQQI--
                                                                                                                                                              DB 2;
C;Superfamily: 4-hydroxyphenylpyruvate_dioxygenase
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                                                                                                                                                              Score 80;
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35; Conservative
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116 INPKIDV 122
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A;Residues: 1-589 <COW>
C;Comment: This S chain,
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                                                                                                                                                      Query Match
Best Local
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T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, Alauthors: Yoshikawa, H.; Zumametein, B.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Reference number: A69580; MUID:98044033; PMID:9384377 A$Accession: B70042 A$ACCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-191 <XUN>
A;Cross-references: UNIPROT:P96502; GB:Z99122; GB:AL009126; NID:g2636029; PIDN:CAB15556
A;Experimental source: strain 168
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C,Superfamily: Bacillus subtilis hypothetical protein yviE
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Best Local Similarity
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Search completed: May 25, 2005, 17:45:25 Job time : 14.1698 secs

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                                                                      brachydanio
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF227660; AAF73401.1; -.

REMBL, AF227260; AAF73401.1; -.

RESP, PA2227; 18G1.

RO; GO:0005634; C:nucleus; IEA.

RO; GO:0000471; F:signal transducer activity; IEA.

RO; GO:0003700; F:transcription factor activity; IEA.

RO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR001217; STAT.

R InterPro; IPR001217; STAT.

R Pfam; PF02161; STAT_alpha; 1.

R Pfam; PF02164; STAT_bind; 1.

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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Signal transducer and activator of transcription (Fragment)
Name=STAT3;
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100.0%; Score 669; DB 2; Length 1
Best Local Similarity 100.0%; Pred. No. 7.6e-55;
Matches 129; Conservative 0; Mismatches 0; Indels
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Q8jfs5
013132
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P40763
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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STR3_BOVIN
STR3_HUMAN
STR3_MOUSE
STR3_RAT
Q6DV79
Q9PVX8
Q7ZXX3
Q7ZXX3
Q7ZXX3
Q6NV46
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Q68D00
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM protein - protein search, using sw model
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Q13133
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Q9QXK0
Q764M5
Q8C497
Q9C3V4
Q9D323
Q8C3W4
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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669
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                           249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
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PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
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                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAN HUMAN STANDARD, PRT, 770 AA.
P40763, O14916; Q9BW54,
O1-FBB-1995 (Rel. 31, Created)
05-JUL-2004 (Rel. 44, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 770;
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05-JUL-2004 (Rel. 44, Created)
5-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
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Homo sapiens (Human).
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DOMAIN 580 670
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                                                                                                Bos taurus (Bovine).
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                                                                             Name=STAT3;
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MOD_RES
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TISSUBERIORE FROM N.A. (ISOFORMS 1 AND DEL-701).

TISSUB-Kidney, and Pancraas;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,

Appleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
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PubMed=11773079; DOI=10.1074/jbc.M11486200;
Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
"Functional interaction of STAT3 transcription factor with the coactivator NCOA/SRC1a.";
J. Biol. Chem. 277:8004-8011 (2002).

J. Biol. Chem. 277:8004-8011 factor that binds to the interleukin-6 (IL-6) responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                            Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T., Yoshida Y., Sudo T., Naruto M., Kishimoto T., "Molatidar cloning of APRF, a novel IFN stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95215843; PubMed=7701321; Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.; Requirement of serine phosphorylation for formation of STAT-promoter
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MEDLINE-98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
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"SeattleSNPs. NHIBH HL6662 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                     TISSUE=Placenta; MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O., "Highly conserved amino-acid sequence between murine STAT3 and revised human STAT3 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acute-phase protein genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 77:63-71(1994).
                                                Mammalia, Euther
NCBI_TaxID=9606;
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730 7
770 AA;
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    CONFLICT
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STA3 MOUSE
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RGO; GO: 000534; C:nucleus; TAS.

RGO; GO: 0005628; F:transcription factor activity; TAS.

RGO; GO: 0005628; F:transcription factor activity; TAS.

RGO; GO: 000529; P:cell motility; TAS.

RGO; GO: 0000122; P:negative regulation of transcription from P. .; TAS.

RGO; GO: 0000122; P:negative regulation of transcription from P. .; TAS.

RGO; GO: 0000125; P:negative regulation of transcription from P. .; TAS.

RGO; GO: 0000125; P:negative regulation of transcription from P. .; TAS.

RGO; GO: 0000125; P:negative regulation; TAS.

RGO; GO: 00001165; P:signal transduction; TAS.

InterPro; IPR009980; SH2.

RICEPPO; IPR001217; STAT.

REAM: PP002864; STAT alpha; 1.

REAM: PP002864; STAT alpha; 1.

REAM: PP002864; STAT alpha; 1.

REAM: PP002865; STAT alpha; 1.
                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-!- PATHWAY: Involved in the gpl30-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1.
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                          ISOUGA-940763-2; Sequence-VSP 010474;
-1- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.
-1- FTM: Tyrosine phosphorylated in response to IL-6, IL-11, CWFF, LIP, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.
-1- SIMILARITY: Belongs to the transcription factor STAT family.
-1- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphotyrosine (by JAK) (By similarity).
Phosphoserine (By similarity).
Missing (in isoform Del-701).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FIId=VSP_010474.
Q -> K (in dbSNP:1803125).
                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR 018679.

Q -> H (in Ref. 1).

P -> S (in Ref. 1).

K -> N (in Ref. 1).

F -> Y (in Ref. 1).

V -> L (in Ref. 1).
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                                                                                                      IsoId=P40763-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                              EMBL, L29277; AAAS8374.1; -.
EMBL, AJ012463; CAA10032.1; -.
EMBL, AX572796; AAS66986.1; -.
EMBL, BC000627, AAH00627.1; -.
EMBL, BC014482; AAH14882.1; -.
EMBL, AF029311; AAB84254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; T01493; -.
Genew; HGNC:11364; STAT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H-InvDB; HIX0013840; -.
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HSSP; P42227; 1BG1.
                                                                                                                  Name=Del-701;
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"Acute phase response factor and additional members of the interferon-
stimulated gene factor 3 family integrate diverse signals from
cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6; Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T., "Molecular cloning of APRF, a novel IRN-stimulated gene factor 3 p91-related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhong Z., Wen Z., Darnell J.E. Jr.; "Stat2s a STAT family member activated by tyrosine phosphorylation in response to epideran growth factor and interleukin-6."; Science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
                                                                                                                                                              Gaps
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STRAIN=BALB/C, and CS7BL/6; TISSUE=Liver;
MEDLINE=96016116; Pubmed=750809;
Schaefer T.S., Sanders L.K., Nathans D.;
"Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                        100.0%; Score 669; DB 1; Length 770; 100.0%; Pred. No. 4.6e-54; ive 0; Mismatches 0; Indels 0
T -> A (in Ref. 1).
; 6C00632211C8012D CRC64;
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SEQUENCE FROM N.A. (ISOFORM STAT3A)
STRAIN=129/SvJ;
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730 T
88067 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/c; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response factor).
Name=Stat3; Synonyms=Aprf;
Mus musculus (Mouse).
                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DKDSGDVAA 129
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Cell 77:63-71(1994).
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REQUENCE FROM N.A. (ISOFORM STAT3A).

SEQUENCE FROM N.A. (ISOFORM STAT3A).

STRAIN=FVB/N. TISSUE-Mammary gland;

MEDINEL-238825; PubMed=12477932; DoI-10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Rapleton M., Soares M.B., Roman D.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabas S.A., McEwan P.J., McKernan R.J., Mark J.D., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Richards A.C., Grimwood J., Schwuchenko Y., Bouffard G.G.,

Rodiguez A.C., Grimwood J., Schwuchenko Y., Bouffard G.G.,

Rodiguez A.C., Grimwood J., Schwuchenko Y., Swailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Robersation and initial analysis of more than 15,000 full-length human

Ry and mouse CDNA sequences "., Red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95554205, PubMed=754, Dol=10.1016/0092-8674(95)90311-9; Wen Z., Zhong Z., Darnell J.E. Jr.; Maximal activation of transcription by Stat1 and Stat3 requires both tyrosine and serine phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOId=P4227-3; Sequence=VSP 010475;
TISSUE SPECIFICITY: STAT3A is Seen in the liver, spleen, and
kidney. STAT3B is also detected in the liver, although in a much
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 394:145-151(1998).
         Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T., Dewar K., Hennighausen L.; "Structure of the mouse stat 3/5 locus: evolution from Drosophila
                                                                                                      STRAIN=CS7BL/6J, and NOD/LLJ;
Davoodi-Semiromi A., She J.-X.;
Ma mutant Stat5b with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
MEDLINE-898334373; PubMed=9671298; DOI=10.1038/28101;
BECKEX S., Groner B., Mueller C.W.;
"Three-dimensional structure of the Stat3beta homodimer bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS
PubMed=11161808; DOI=10.1006/geno.2000.6433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P42227-2; Sequence=VSP_006287;
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                                                                                            SEQUENCE FROM N.A. (ISOFORM STAT3A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."
                                                                 Genomics 71:150-155(2001).
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                                                     zebrafish to mouse."
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TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
FDMDLTSECATSPM -> FIDAVWK (in isoform
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                    homodimers and maximal transcriptional activity (By similarity). SIMILARITY: Belongs to the transcription factor STAT family. SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                               EMBL; 1029278; AAA19452.1; --

BERL; 106922; AAA19452.1; --

BERL; 106922; AAA19452.1; --

BERL; 108778; AAA56668.1; --

BERL; 108778; AAA55668.1; --

BERL; 47299489; AAA55418.1; --

BERL; 47299489; AAA75418.1; --

BERL; 47299489; AAA75419.1; --

BERL; 47299489; AAA75419.1; --

BERL; A7299489; AAA77419.1; --

BERL; A74744007; ACUTE phase; Alternative splicing; BERL; BERL; BAY7419.1; BAY7419.1
is important for the formation of stable DNA-binding STAT3
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/FTId=VSP 010475.
S->A: Decreased transcriptional
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S -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
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/FTId=VSP 006287
                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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                                                                                                                                                                                              249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
                                                                                                                                                                                                                                                                                      309 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVKUI 368
                                                                                                                                                                                                                                                          61 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fey G.H., "Transcription factors Stat3 and Stat5b are present in rat liver "Transcription factors Stat3 and Stat5b are present in an acute phase response and bind interleukin-6 response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 270:29998-30006(1995).
-!- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                     1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Liver;
MEDLINE-96102059; PubMed-8530402; DOI=10.1074/jbc.270.50.29998;
Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.
                                                                                Length 770;
                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                              100.0%; Score 669; DB 1;
100.0%; Pred. No. 4.6e-54;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         770 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X91810; CAA62920.1; -.
                                                                                                     Best Local Similarity 100.0
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                    121 DKDSGDVAA 129
                                                                                                                                                                                                                                                                                                                                                                                 DKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Stat3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STA3 RAT
P52631;
                                                                                Query Match
                                    STRAND
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RGD; 3772; Stat3. InterPro; IPR008967; P53\_like\_DNA\_bnd. InterPro; IPR000980; SH2.

InterPro; IPR001217; STAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IVELFRNIAMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                 similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                            SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.4%; Score 665; DB 2; Length 771; 99.2%; Pred. No. 1.1e-53; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                       Phosphotyrosine (by JAK) (By Phosphoserine (By similarity) D74A0C76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou G.Y., Leung F.C.,
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal transducer and activator of transcription 3.
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8.7e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                770 AA; 88039 MW;
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT_bind; 1.
SMART; SM00252; SH2; 1.
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.2%;
                                                                                                                                                                                                                                                                                                                   Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 771 AA;
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Kenopus laevis (African clawed frog)
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 309 IVELFRNLMKSAFVVERQPCMPMHPDRPLVFKTGVQFTTKVRLLVKFPELNYQLKIKVCI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                  MEDIINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518; Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T., Asashima M., Yokofa T.; Matsivation of Stata Dy cytokine receptor gpl30 ventralizes Xenopus embryos independent of BMP-4.";
                                                                                                                                                                                                                                                                                                                 GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR0009867; SH2.
InterPro; IPR0009867; SH2.
                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Cranīata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.4%; Score 658; DB 2; Length 769; 98.4%; Pred. No. 4.9e-53; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               769 AA; 87974 MW; 0905C03263303069 CRC64;
                                                                                                                        Last sequence update)
Last annotation update)
                                                                                            769 AA.
                                                                                                                Created)
                                                                                                                                                        Name=stat 3;
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00017; SH2; 1.
Pfam; PF01017; SH2 alpha; 1.
Pfam; PF02864; STAT alpha; 1.
Pfam; PF02865; SHAT int; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                       Dev. Biol. 216:481-490(1999).
EMBL; AB017701; BAA86061.1; -.
                                                                                                               01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                          interPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 127; Conservative
                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKDSGDVAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKDSGDVAA 377
                       DKDSGDVAA 129
                                                                                                                                                                                                Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                            HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                           DKDSGDVAA
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=8355;
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                      121
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                                           369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                Stat 3.
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                                                                         RESULT 7
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Q7ZXK3 PRELIMINARY; PRT; 766 AA. Q7ZXK3; Q1-ZXK3; Q1-JUN-2003 (TrEWBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) Stats-2004 (TrEMBLrel. 26, Last annotation update) Name=stat3-A;

GERTAGE

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A STANDER S. S. Pebbwed-12477932; DOI=10.1073/pnas.242603899;

RA STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Wagner L., Sheamen C.W., Schuler G.D.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M. Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA BROWS S.A., McEwan D. B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA BROWS S.A., McEwan D.J., McKernan K.J., Male J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA BROWS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RAT "Generation and initial analysis of more than 15,000 full-length human and mouse cuna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0003724; F:signal transducer activity; IEA.

R GO; GO:0007242; P:intracellular signaling cascade; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR008967; P53_like_DNA_bnd.

R InterPro; IPR001917; SH2.

R Pfam; PF00017; STAT.

R Pfam; PF00864; STAT_alpha; 1.

R Pfam; PF02865; STAT_bind; 1.

R Pfam; PF02865; STAT_int; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 IACIGGPPNICLDRLENWITSLAESQLQTRQQIRKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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97.2%; Score 650; DB 2; Length 76
Best Local Similarity 96.9%; Pred. No. 2.7e-52;
Matches 125; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO44717; AAH44717.1; -.
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87599 MW; 31018A3321CCEB9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dev. Dyn. 225:384-391(2002).
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PROSITE; PS50001; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   766 AA;
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                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=8355;
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us-10-090-185-24.rup

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310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI 369
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT_int; 1.
                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 121; Conservative
                                                                                PRELIMINARY;
                              ||:||||||
DKESGDVAA 378
                  121 DKDSGDVAA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             786 AA;
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                           Stat3 protein.
                                                                                                                                                                                                           rissum=Kidney
                                                                                                 05-JUL-2004
05-JUL-2004
                                                                                                                                      Name=stat3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                           Q6NV46;
                                                                               Q6NV46
                                                              RESULT 10
Q6NV46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000155; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008967; P53 like_DNA_bnd.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.2%; Score 637; DB 2; Length 414; 93.8%; Pred. No. 2.2e-51; ive 5; Mismatches 3; Indels
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO45275; AAH45276.1; --
HSSP; P42227; 1BG1.
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AA: 48253 MW; OFFD1B509B7526BD CRC64;
                                                                                       01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                              414 AA.
                                                                               Created)
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Pfam; PF02864; STAT bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                             01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity ....
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
                                                             PRELIMINARY;
DKDSGDVAA 129
                369 pkpscegaa 377
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                                                                                                                                                       Danio.
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                    Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                          Stat3 protein.
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                                                                                                                    Name=stat3;
121
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                                                             Q7ZTS5
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RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altachuls R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Rapleron M., Soarsen M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rapas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Raha S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Shevchenko Y., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., Smailus D.E., Schmerch A., Schein J.E., Schmerch 
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A Strausberg R.;

Rems.; BC068320; A4468320.1; -..

R ZFIN; ZDB-GENE-980526-68; stat3.

R GO; GO:000451; F:signal transdering to according t
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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786 AA
PRT;
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Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
                                                                                                                                                       NCBI_TaxID=8090;
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Best Local 8
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                                                        IVELFRNLMKSAFVVERQPCMDMHPDRPLVIKTGVQFTTKVRLLVKFPELMYQLKIKVCI
                                                                                           A dates A.C.;

I Thesis (1998), University of Melbourne, Australia.

I Thesis (1998), University of Melbourne, Australia.

I REMBL; A0005293; CAA06677.1;

R RSPP; P42227; 18G1.

R GO; GO:0004871; F:signal transducer activity; IEA.

R GO; GO:0007242; P:signal transducer activity; IEA.

R GO; GO:0008700; F:transcription of transcription, DNA-dependent; IEA.

InterPro; IPR00980; SH2.

InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygil; Neopterygil; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 4.8e-51;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Signal transducer and activation of transcription factor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74BC4EA401C3C942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Danio rerio).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350001; SH2; 1.
806 AA; 92151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
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08,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                          370 DKESGDVAA 378
                                                                                                                                                                                 DKDSGDVAA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription factor.
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PROSITE; PS50001; SH
SEQUENCE 806 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Matches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6DVF3
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093599
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310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTNKVRLLVKFPELNYQLKIKVCI 369
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R GO; GO:0004871; F:AT64912.1; -.

GO; GO:0004871; F:AT64912.1; -.

GO; GO:0004871; F:Signal transderivity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:00005285; P:requilation of transcription, DNA-dependent; IEA.

InterPro; IPR008967; P53 like_DNA_bnd.

InterPro; IPR001207; STAT.

R Pfam; PF00017; STAT.

R Pfam; PF00017; STAT alpha; I.

R Pfam; PF00107; STAT alpha; I.

R Pfam; PF02864; STAT bind; I.

R Pfam; PF02865; STAT int; I.

R Pfam; PF02865; STAT int; I.

R Pfam; FR02865; STAT int; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Signal transducer and activator of transcription 3 isoform 1.
Signal transducer and activator of transcription 3 isoform 1.
Eukaryota; Medaka fish) (Japanese ricefish).
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
NCBL_TaxID=8090;
                                                        Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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Submitted (MAY-2004) to the EMEL/GenBank/DDBJ databases.

EMBL, AY641434, AAT46364.1;

GO, GO:0006534; C:nucleus; IEA.

GO, GO:0004871; F:signal transducer activity; IEA.

GO, GO:0007242; F:transcription factor activity; IEA.

GO, GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR009867; PS3_like_DNA_bnd.
                                 Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                        Liu R., Hong Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 635; DB 2;
Pred. No. 7e-51;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   785 AA.
                             Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
Oryzias latipes (Medaka fish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.9%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 93.8 Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:||||||
|DKESGDVAA 378
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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767 AA

PRELIMINARY;

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Stat3
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                                                                                                               250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIKKLEELQQKVSYKGDPIIQHRPALEEK 309
                                                                                                                                                  120
                                                                                                                                                             250 IACIGGPPNICLDRLETWITSLAESOLOIRQOIKKLEELQOKVSYKGDPIIQHRPALEEK 309
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                                                                                                1 IACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                               61 IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCI
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                         Tetraodon fluviatilis (Puffer fish).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Butaryota; Meopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.

MCBI_TaxID=47145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 764;
                                                Length 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.3%; Score 624; DB 2; Length 76
92.2%; Pred. No. 7.5e-50;
ive 5; Mismatches 5; Indels
                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307106; AAL09415.1; -.
HSSP; 942227; 18G1.
                   89643 MW; 81F231BDB27DB938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87411 MW; E661FFE18BEFD8BE CRC64;
                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                               Score 635; DB 2;
Pred. No. 7.2e-51;
4; Mismatches 4;
                                                                                                                                                                                                                                                                                    764 AA.
                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SMART; SM00252; SH2; 1.
                                                94.9%;
93.8%;
Pfam; PF02865; STAT int; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 785 AA; 89643 MW
                                            Query Match
Best Local Similarity 93.8°
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 92.2
Matches 119; Conservative
                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                 DKDSGDVAA 129
                                                                                                                                                                                                              ||:||||||
DKESGDVAA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|||||:
||SESGDVAS 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKDSGDVAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 764 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00252; SF
PROSITE; PS50001;
                                                                                                                                                                                                                       370
                                                                                                                                                                                                121
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Q90Y16
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RESULT 15 013133

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 IACIGGPPKICLDRLETWITSLGEIQLQIRQQIKKLEELQQKVSYKGDPIIQHRPALEEK 309
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                                                                                                                                                                                                                                                                                                                           Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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89.7%; Score 600; DB 2; Length 767;
Best Local Similarity 89.9%; Pred. No. 1.3e-47;
Matches 116; Conservative 4; Mismatches 9; Indels
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U60333; AAB60926.1; -.
HSSP, P42227; 1BG1.
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Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT int; 1.
Pfam; PF02865; STAT int; 1.
SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;
                                                                                                                          Last sequence update)
Last annotation update)
                                                                Created)
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                                                          01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2004 (TrEMBLrel. 26,
                                                   (TrEMBLrel.
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013133;
01-JUL-1997
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Mouse Sta Mouse Sta Mouse Sta Mouse Sta Rat STAT-Mouse Sta Human tru

Mouse

Human exp Truncated

sig ISG

Human 84 kD Human Human

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/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
Aay72861 Nay72862 Nay72862 Nay72862 Nay72862 Nay72862 Nay72866 Nay72861 Nay72861 Nay72864 Nay72866 Nay72864 Nay72866 Nay72864 Nay72866 Nay72864 Nay72866 Nay7286 Nay728 Nay
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                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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AAY72846
AAY72846
AAY72851
AAY72847
AAA72847
AAA62296
AAM62996
ABR59713
ABR69747
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WPI; 2001-226705/23.
WO200116605-A2
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                                                                                            May 25, 2005, 17:14:45 ; Search time 51.0983 Seconds (without alignments) 726.619 Million cell updates/sec
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1 KKLBELQQKVSYKGDPIVQH......LNYQLKIKVCIDKDSGDVAA
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Aay72855
Aay72864
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Aac22055
Aar22095
Aar22092
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             2105692 seqs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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AAR72082
AAR82995
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AAE14652
ABG69497
ABU10476
ADN04365
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AAE22054
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ADD44738
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geneseqD2000s:*
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/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
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                                                                                                                                                 Gaps
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                                                                                                    Length 96;
                                                                                                                                             Indels
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                                                                                                  ; Score 494; DB 4;
; Pred. No. 3.6e-55;
0; Mismatches 0;
                                                                                                                                                                                                                                                                       GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
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transcription factor
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                                                                Sequence 96 AA;
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/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse Stat3 protein fragment #13 (193-377 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Darnell JE;
                                                                                                                                          94 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 129
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100.0%; Pred. No. 8.4e-55;
ive 0; Mismatches 0;
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                                                                                                                   GVOFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA
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                                                                                                                                                                                                                                                                                                                      AAY72855 standard; protein; 185
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96; Conservative
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AAY72854;

therapy

Key Region

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The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a franscription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for treating cancer and psortiasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                             236. .252
/note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
                                                                                                                                         Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                     Mouse Stat3 protein fragment #2 (107-377 amino acids).
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100.0%; Pred. No. 1.4e-54;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang X, Horvath C, Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 65; Page 67-68; 86pp; English.
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                                                                (first entry)
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                                                                31-MAY-2001
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                          AAY72841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is mouse Stat3 protein fragment containing 155-377 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                       corresponds to
                                                                                                                                                                                                                                                                           Mouse, Stat3 protein, transcription factor, c-Jun; gene transcription, cellular transformation, dysproliferative disease, cancer; psoriasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                   188. .204
/note= "Stat3-c-Jun interaction region 2;
342-358 position of Stat3 protein"
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                                                                                                                                                                                                                                       Mouse Stat3 protein fragment #12 (155-377 amino acids).
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100.0%; Score 494; DB 4;
100.0%; Pred. No. 1.1e-54;
tive 0; Mismatches 0;
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188. .204
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                                                                                                                     AAY72854 standard; protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2000; 2000WO-US023822
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Les 96; Conserv
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08-MAR-2001

Zhang X,

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RESULT 5 AAY72841 ΩI

Query Match

Best Loc Matches

Length 271; Indels Stat3beta protein

SXS

Sequence 720 AA;

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25-JUL-2002 (first entry)
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Human Stat3beta protein.

Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypostia; stroke; anglogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative anglopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple scleroais; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.

Homo sapiens

Key Misc-difference 713. .714 /note= "Encoded by ACA CCA TTC"

WO200220032-A1

14-MAR-2002

10-SEP-2001; 2001WO-US028254.

08-SEP-2000; 2000US-0231212P

(UYSF-) UNIV JOHNS HOPKINS. (UYSF-) UNIV SOUTH FLORIDA.

Jove R, Dalton W; Pardoll D, 'n H,

WPI; 2002-362218/39. N-PSDB; AAD35066.

Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator transcription 3.

Disclosure; Page 87-89; 94pp; English

The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription of 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, mycoardial infarction, inflammation, tisque ischaemia in the lower extremities, infarction, inflammation, crisque ischaemia in the lower extremities, infarction, inflammation, crisque ischaemia in the lower extremities, infarction, usiffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hyposlycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, introgen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematogus, multiple sclerosis, insulin dependent diabetes mellitus, cardinorating a symptom of an autoimmune disease such as systemic lupus erythematogus, multiple sclerosis, insulin dependent diabetes mellitus, mixed connective tissue disease, primary biliary cirrhosis pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, cliopathic thrombocytopenia purpura, Grave's disease, vitiligo, cliopathic thrombocytopenia purpura, Grave's disease, cliopature eneropathy, autoimmune neutropenia, mysthemia gravis, cliopathic thrombocytopenia purpura, Grave's disease, cliopature, and oncoganic disease which includes sarcomes and carcinomas e.g., bladder carcinoma, colon carcinoma, cliopatic proliferative and oncoganic disease which includes sarcomas and carcinoma e.g., bladder carcinoma, clon carcinoma, chromic leveamia, physoroliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases, AB199913 and AB19914 represent PCR thrapeutics for ischaemic descaes, AB19913 and AB19914 represent pcreamin the exemplification of the present invention

Claim 2; Page 1084-1087; 2690pp; English.

Score 494; DB 5; Length 769; Pred. No. 5.3e-54;

100.0%; 100.0%;

Query Match Best Local Similarity

Sequence 769 AA;

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                                                          282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                             1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                       Gaps
                                                                                                                                                                                                                                                  Mouse ischaemic condition related protein sequence SEQ ID NO:398
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                                                                                                                                                                                                                                                                          Mouse, ischaemia, compressive ischaemia, occlusive ischaemia, vasospastic ischaemia, ischaemic condition, ischaemic disease.
Length 720;
                       Indels
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                                                                                                          342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
100.0%; Score 494; DB 5;
100.0%; Pred. No. 4.8e-54;
iive 0; Mismatches 0;
                                                                                            61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
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                                                                                                                                                                                                                              (first entry)
                       96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-034733/04.
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                  282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
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                                          1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; anglogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; inflammation; chronic obstructive pulmonary disease; cardiac arrest; shock; chronic active hepatitis; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; theumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; signal transducer and activator of transcription 3; ischaemia;
  Indels
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Mismatches
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(UYSF-) UNIV SOUTH FLORIDA.
                                                                                                                                                                                                                                                                                                                                                               25-JUL-2002 (first entry)
96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         Human Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription 3.
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                                                                                idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, theumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative collits and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and earchingas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, bhysical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis, maked connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia, stroke; angiogenesis; myocardial infearction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                          'Match 100.0%; Score 494; DB 5; Length 769; Local Similarity 100.0%; Pred. No. 5.3e-54; les 96; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein related to angiogenesis regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dalton W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE22056 standard; protein; 769 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-2001; 2001WO-US028254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000; 2000US-0231212P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS. (UYSF-) UNIV SOUTH FLORIDA.
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                                                                                                                                                                                                                                                                                                                                   Sequence 769 AA;
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A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339-40) were cloned in plasmids 13sfl and 19sf6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNIMKSAFVVERQPCMPMHPDRPLVIKT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                                                                     Receptor recognition factor implicated in transcriptional stimulation genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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100.0%; Pred. No. 5.3e-54;
ive 0; Mismatches 0;
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                                                                                                                              Wen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse liver acute phase response factor.
                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 107-110; 160pp; English.
                                                                                                                              Shuai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR82995 standard; protein; 770 AA
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  94US-00212184.
94US-00212185.
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                                                                                                                            Schindler CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003 to correct PN field.)
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                                                                            (UYRQ ) UNIV ROCKEPELLER
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                                                                                                                                                                           WPI; 1995-139598/18.
N-PSDB; AAQ89340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 770 AA;
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11-MAR-1994;
11-MAR-1994;
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                                                                                                                              Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1996
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                                                                                 The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that response. Method involves administering to an individual a compound that compound the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemia on angiogenesis is weeful for treating or preventing the consist of the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tischaemia, vaccular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, applyse, and angiogenty e.g. diabetic microangiopathy introgen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, signared connective elecase, primary biliary cirrhosis, pernicious maxemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, dirrhosis, pemphigus vulgaris, autoimmune cinfertility, bullous pemphigoid discoal lupus, ulcerative colitis and ensering carreling and carreling and carreling and ensering coliferative and oncogenic disease, which in preventing or treating corrections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein related to angiogenesis regulation
                                               Disclosure; Page 83-85; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR72082 standard; protein; 770 AA.
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93US-00126595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Stat3 (19sf6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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24-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9508629-A1
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27-SEP-1995
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RESULT 10 AAR72082 Mus sp.

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Length 770; Indels

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Sequence 770 AA;
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                                                                                                                                                                                                                                                                                                                                    11-JUN-1999
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                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                       RESULT 13
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                                                            transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a CDNA, isolated from a mouse liver CDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. PARF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
                                                                                                                                                                                                                               KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
                                                                                                                                                                                                                  KKLEBLQQKVSYKGDPIVQHRPMLEERIVELFRNIMKSAFVVBRQPCMPMHPDRPLVIKT 60
diseases induced by cytokine(s) such as IL-6, e.g. inflammatory

    useful for diagnosing,
    oncogenesis,

                                                   sequence represents a mouse acute phase response factor (APRF), a
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse signal transducer and activator of transcription (STAT) protein
                                                                                                                                                                                                                                                                                                                                                                                                                   4; signal transducer and activator of transcription; g protein; ligand; receptor; oncogenesis; inflammation; disease; antagonist; therapy.
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                                                                                                                                                                           100.0%; Score 494; DB 2; Length 770; 100.0%; Pred. No. 5.3e-54; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New STAT protein DNA-binding domain peptide(s) - u preventing or treating cellular dysfunction, e.g. inflammation, parasitic disease or autoimmunity.
                                                                                                                                                                                                                                                                       GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                            GVOFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398. .508
/label= DNA binding domain
/note= "Claim 3, page 110"
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                               Page 20-22; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wen Z, Horvath CM,
                                                                                                                                                                                                                                                                                                                                   AAW03176 standard; protein; 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95WO-US017025
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-333941/33.
                                                                                                                                    hypertension, etc
                                                                                                                                                       Sequence 770 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9620954-A2
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                                                                                                                                                                                                                                                                                                                                                                           24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                            DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                Mouse STAT4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune
                               Claim 10;
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                                                                                                                                                                                                                                                                                                                                                        AAW03176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. The encoding sequence differs from the original published human STAT3 gene sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3 DAM molecule can be used for the recombinant expression of the variant. STAT3 protein is useful as a medicament or pharmaceutical composition for treatment of autoimmune or inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery vi DNA binding in a receptor-ligand specific manner. STAT proteins and the binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and activation of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KKLEELQOKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 494; DB 2; 100.0%; Pred. No. 5.3e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human STAT3 allelic variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
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N-PSDB; AAX29281.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.
                                 1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                   Gaps
                                                                                                                                                                                               transducer and activator of transcription; crystal; murine.
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 Length 770;
                  Indels
                                                                                                                                                                                                                                                                                           alpha helix 2
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                                                                             GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
1100.0%; Score 494; DB 2;
1100.0%; Pred. No. 5.3e-54;
ive 0; Mismatches 0;
                                                                  GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                              N-terminal domain of murine STAT-3 protein.
                                                                                                                                                                                                                                                                                 Darnell JE,
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/label= Alpha helix 1
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|Tabel= Alpha helix 2
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/label= Alpha helix 7
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/label= Alpha helix 8
                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                            AAB12377 standard; peptide; 770 AA.
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                 96; Conservative
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         Similarity
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                                                                                                                                                                                               STAT; signal
drug design;
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than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that enhances or diminishes the binding of the dimeric STAT protein, to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the binding of the STAT protein to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new

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/note= "Conserved N-terminal domain of the STAT family"

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                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying compounds that bind to signal transducer and activat transcription proteins, useful for the production of new drugs.
                                                                                                                                                                        Length 770;
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                                                                                                                                                                    100.0%; Score 494; DB 3;
100.0%; Pred. No. 5.3e-54;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE14652 standard; protein; 770 AA
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                                                                                                                                                                                       Similarity 100.0%;
96; Conservative 0
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                                                                                                                                 Sequence 770 AA;
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The present invention relates to a crystal of an N-terminal fragment of signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-95-091-12
US-08-956-65-12
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US-09-912-710-8
US-09-956-65-12
US-09-364-970-3
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US-09-972-800A-6
US-08-276-099A-14
US-08-781-890-14
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                                                                                                             OM protein - protein search, using sw model
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No.
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Cutr M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
FILE REPRENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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US-09-387-418A-18
US-09-387-418A-28
US-09-387-418A-31
US-09-387-418A-14
US-09-387-418A-14
US-09-387-418A-15
US-09-387-418A-15
US-09-387-418A-15
US-09-387-418A-15
US-09-387-418A-15
US-09-387-418A-15
US-09-36-66-6
US-08-36-796-6
US-08-26-65-6
US-08-956-65-6
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APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Barnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-223
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-387-418A-25; Sequence 25, Application US/09387418A; Sequence 25, Application US/09387418A; Patent No. 6391572; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/09387418A; Patent No. 6391572; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 96; Conservative
GRANISM: Mus musculus
US-09-387-418A-25
  RESULT 2
US-09-387-418A-24
  3396
3396
3396
3310
3310
3310
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LENGTH: 96
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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-23
CURRENT FILING DATE: 199-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: James B. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: TRANSDUCER AND ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT)
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMFWHPDRPLVIKT 187
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                                                                                                                                                                                                                                                                                                                                                  188 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 223
                                                                                                                100.0%; Score 494; DB 3;
100.0%; Pred. No. 1.3e-53;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-53;
Matches 96; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                      61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 9, Application US/09387418A; Patent No. 6391572; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 12, Application US/08369796; Patent No. 5716622; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 271
TYPE: PRT
ORGANISM: Mus musculus
                                       ; ORGANISM: Mus musculus
US-09-387-418A-22
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US-08-369-796-12
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US-09-387-418A-9
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APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT PRILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESCRIPTION OF 1987-418A-22
Sequence 22, Application US/09387418A
GENERAL INFORMATION:
APPLICANT: Waresaczynska, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: NETHORS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 223
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                                                                                                                                                                                                                                                                                                                           34 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 93
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                                                                                                                                                                                              Query Match 100.0%; Score 494; DB 3; Length 129; Best Local Similarity 100.0%; Pred. No. 6.3e-54; Matches 96; Conservative 0; Mismatches 0; Indels
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100.0%; Score 494; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 1e-53;
Matches 96; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           GVOFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 129
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                       PatentIn Ver. 2.0
                                                                                                                     ; ORGANISM: Mus musculus US-09-387-418A-24
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SOFTWARE: Pate
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-387-418A-23
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                                                                                             TYPE: PRT
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Sequence 12, Application US/08852091

Patent NO.588328

GENERAL INFORMATION:

APPLICANT: James E. Darnell, Jr.

APPLICANT: Curt M. Horvath

APPLICANT: Curt M. Horvath

APPLICANT: Curt M. Horvath

APPLICANT: Curt M. Horvath

APPLICANT: The OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL

TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS

CORRESPONDENCE ADDRESS: 39

CORRESPONDENCE ADDRESS: Jackson

STREET: 411 Hackensack Avenue

GITY: Hackensack

GITY: Hackensack

GITY: Hackensack

GITY: Hackensack

GITY: Hackensack

GITY: Hackensack

GITY: Hackensack
                                                                                                                                                                                                                                                                                      282 KKLBELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
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                                                                                                                                                                                                                                                     1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
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                                                                                                                                                          Length 770;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-MAY-1995
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                     100.0%; Score 494; DB 1;
100.0%; Pred. No. 6.4e-53;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                     61 GVOFTTKVRLLVKPPELNYQLKIKVCIDKDSGDVAA 96
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Pred. No. 6.4e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.0%; Pi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
     : 770 amino acids
amino acid
                                                                                                                                      Query Match
Best Local Similarity 100.0
....hes 96; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                           ; MOLECULE TYPE: protein US-08-416-5818-9
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                                                TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTEXT ADDRESSES
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
RION APPLICATION 1435
PRING DATE: 04-APR-1994
FILING DATE: 04-APR-1994
FILING DATE: 04-APR-1994
ATTONENY/APRATION: PG-201
                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08416581B
Patent No. 5719042
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Rishimoto, Tadamitsu
APPLICANT: Rishimoto, Tadamitsu
APPLICANT: ALIANSCRIPTION FACTOR APRF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SE
                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Jacken Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFRX: 201 347-5800
TELERX: 201 343-1684
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REGISTRATION INDRER: Q-37891
TRELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                           PC-DOS/MS-DOS
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                  i LENGTH: 770 amino acids

i TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-369-796-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 96; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-416-581B-9
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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Ann, Zilong
APPLICANT: Anny Zhong
APPLICANT: Anny Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                          342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                           RESULT 10
US-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
COUNTRY: USA
ZID: ACCOUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 494; DB 2; Length 770; 100.0%; Pred. No. 6.4e-53; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER TEADABLE PORM:

MEDIUM TYPE: Floppy disk

COMPUTER ISM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 11-MAR-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRILING DATE: 19-MAR-1993
FILING DATE: 19-MAR-1993
FILING DATE: 19-MAR-1993
FILING DATE: 24-SEP-1993
                                                                                     61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600-1-073 CIP
                                                                                                                                                                                                                                                  US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent No. 5976835
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
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                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 494; DB 3;
100.0%; Pred. No. 6.4e-53;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Egg., David A.
REGISTRATION NUMBER: 26,742
REPERBRICE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                             APPLICATION NUMBER: US/US/999,032
FILING DATE:
RIOR APPLICATION:
PRIOR APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-5EP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPWHPDRPLVIKT 341

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Query Match
Best Local Similarity 100.0
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                        CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 411
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US-08-948-547-12
                                                      US-09-012-710-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                               Sequence 12, Application US/08956869
Patent No. 6030808
GENERAL INFORMATION:
APPLICANT: Schindler, Christian W. APPLICANT: Schindler, Christian W. APPLICANT: Fu, Xian-Yuan APPLICANT: Fu, Xian-Yuan APPLICANT: Pong, Zhong APLICANT: Zhong APPLICANT: Zhong APPLICANT: Schong, Sequences AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
342 GVOFTTKVRLLVKFPELNYQLKIKVCIDKOSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGBVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 494; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMINICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-8EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 770 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-956-869-12
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07601
                                                                                                               -08-956-869-12
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282 KKLEBLQQKVSYKGDPIVQHRPMLEBRIVELFRNIMKSAFVVBRQPCMPMHPDRPLVIKT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KKLEELQOKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                         APPLICANT: Vinkemeier, Uwe
APPLICANT: Vinkemeier, Uwe
APPLICANT: Vinkemeier, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Marial
APPLICANT: Wariyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 494; DB 3; Length 770; 100.0%; Pred. No. 6.4e-53; ive 0; Mismatches 0; Indels
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Patent No. 6124118
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
APPLICANT: Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE:
CLASSIFTCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCY/DOCKET NUMBER: 26,742
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEFAX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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                                                                                                                                                                                                                                                                                                                E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
; Sequence 8, Application US/09012710; Patent No. 6087478; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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Indels

Length 770;

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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMFWHPDRPLVIKT 341
                                                                                                                                                                                          1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                                                                                                                 342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                               100.0%; Score 494; DB 3;
100.0%; Pred. No. 6.4e-53;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                              US-09-364-970-5; Sequence 5, Application US/09364970; Patent No. 6235873
                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-5
SEQ ID NO 3
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
                                                                              US-09-364-970-3
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                                                                                                                     ZIP: 07601

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION 1487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                  PRICE APPLICATION:
PRICE APPLICATION:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRICE APPLICATION DATE:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRICE APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 0833/02569
FILING DATE: 19-MAR-1993
FILING DATE: 24-SEP-1993
ATTORNEY, AGENT INFORMATION:
                        ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-948-547-12
      CORRESPONDENCE ADDRESS:
                                                                                  STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
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Sequence 3, Application US/09364970

Sequence 3, Application US/09364970

Patent No. 6235873

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
FILE REPERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970

CURRENT PILING DATE: 1999-07-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0

US-09-364-970-3

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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
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GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS
FILE REPERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT PILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SSETURE REPERENCE: OF SEQ ID NOS: 10
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Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0;
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May 25, 2005, 17:36:58 ; Search time 42.0417 Seconds (without alignments) 763.830 Million cell updates/sec
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1 KKLEBLQQKVSYKGDPIVQH.....LNYQLKIKVCIDKDSGDVAA 96
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(gnz_6/ptodata/2/pubpaa/US07 PUBCOMB.ppp:*

(gnz_6/ptodata/2/pubpaa/US06 PUBF PUB.ppp:*

(gnz_6/ptodata/2/pubpaa/US06 PUBCOMB.ppp:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1434725 seqs, 334507595 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications_AA:*
                                                                                                                                                                           OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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116:
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119:
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		% Query				
	Score	Match	Match Length DB	DB	ID	Description
! !	494	100.0	96	13	US-10-090-185-25	
	494	100.0		13	US-10-090-185-24	
	494	100.0		13	US-10-090-185-23	
	494	100.0		13	US-10-090-185-22	Sequence 22, Appl
	494	100.0		13	US-10-090-185-9	Sequence 9, Appli
	494	100.0		15	US-10-380-020-4	Sequence 4, Appli
	494	100.0		15	US-10-380-020-2	7
_	494	100.0		15	US-10-380-020-5	Sequence 5, Appli
_	494	100.0		11	US-09-876-773-12	12,
_	494	100.0	770	14	US-10-045-792-8	8
	494	100.0		14	US-10-038-010-56	Sequence 56, Appl
	494	100.0		14	US-10-117-087-2	Sequence 2, Appli
_	494	100.0		17	US-10-639-617-12	Sequence 12, Appl

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	30, 31, 29, 19, 15,	7 66269	4 4 4 6 6 4	Sequence 4, Applia Sequence 550, App Sequence 437, App Sequence 439, App Sequence 70, Appl Sequence 362, App
	13 US-10-090-185-30 13 US-10-090-185-31 13 US-10-090-185-19 13 US-10-090-185-19 13 US-10-090-185-19 13 US-10-090-185-15 9 US-09-833-205-4	13 US-10-090-185-12 14 US-10-245-120-3 11 US-09-876-773-6 14 US-10-245-120-2 17 US-10-639-617-6 17 US-10-936-390-5 9 US-09-833-205-2	11 US-09-876-773-4 14 US-10-245-120-1 14 US-10-308-279-44 16 US-10-755-889-352 16 US-10-755-889-823 17 US-10-492-043-19	1 US-10-639-61.7-4 9 US-09-925-297-550 14 US-10-177-293-433 14 US-10-177-293-439 16 US-10-755-889-70 16 US-10-755-889-362
793 770 770 229	229 229 252 229 213 749	268 582 712 712 712 750	750 750 750 750 750	786 7423 748 748
100.0 100.0 99.4 80.2	880 780 780 780 780 780 780 780 780 780	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0.02.03.03.03.03.03.03.03.03.03.03.03.03.03.	5 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9
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## ALIGNMENTS

US-10-090-185-25

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Sequence 25, Application US/10090185
; Sequence 25, Application US/20020197647A1
; GENERAL INFORMATION:
    APPLICANT: Zhang, Xiaokui
    APPLICANT: Zhang, Xiaokui
    APPLICANT: Thang, Xiaokui
    APPLICANT: Horvath, Curt M
    TITLE OF INVENTION: INTERACTIONS
    TITLE OF INVENTION: INTERACTIONS
    TITLE OF INVENTION UNMER: US/10/090,185
    CURRENT FILING DATE: 2002-03-04
    PRIOR APPLICATION NUMBER: 09/387,418
    PRIOR FILING DATE: 1999-08-31
    NUMBER OF SEQ ID NOS: 43
    SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mus musculus
US-10-090-185-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 25
LENGTH: 96
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wzeszczynska, Melissa H
APPLICANT: Wzeszczynska, Melissa H
APPLICANT: Wzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-233
CURRENT APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION NUMBER: 09/387,418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/10090185
Publication No. US2002019764741
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Abrag, Xiaokui
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
ITILE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
ITILE OF INVENTION: INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 235
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Pred. No. 8.5e-53;
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CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
                                              Sequence 22, Application US/10090185 Publication No. US20020197647A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
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US-10-090-185-22
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Best Local Similarity
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Best Local Similarity
Matches 96; Conserv
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LENGTH: 223
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                                                                                                                  APPLICANT: WIZESZCZYNEKA, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR ITLLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT PILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION OFF: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Mrzeszczynaka, Melissa H
APPLICANT: Mrzeszczynaka, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR ITILE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-223
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-30-4
PRIOR FILING DATE: 1999-08-31
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100.0%; Score 494; DB 13;
Best Local Similarity 100.0%; Pred. No. 6.7e-53;
Matches 96; Conservative 0; Mismatches 0;
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                    Sequence 24, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
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SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Mus musculus
US-10-090-185-23
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US-10-090-185-24
-10-090-185-24
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LENGTH: 185
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GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 271

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APPLICANT: Yu, Hua
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 769
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 494; DB 15;
100.0%; Pred. No. 4.2e-52;
iive 0; Mismatches 0;
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APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09876773; Publication No. US20040058318A1; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
'MEDIUM TYPE: Floppy disk
                    ; Sequence 5, Application US/10380020; Publication No. US20040052762A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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STATE: New Jersey
COUNTRY: USA
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Best Local Similarity 100.
Matches 96; Conservative
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; ORGANISM: Homo Sapiens
US-10-380-020-5
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US-10-380-020-5
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                                                                                                 SCHERENT IN TAXABLE AND STATE APPLICANT: YU, Huan APPLICANT: Pardoll, Drew APPLICANT: Pardoll, Drew APPLICANT: Dalton, Willian ITILE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof FILE REFERENCE: 10873-009-999 CURRENT APPLICATION NUMBER: 10873-009-999 CURRENT FILING DATE: 2003-03-07 PRIOR APPLICATION NUMBER: 60/231,212 PRIOR APPLICATION NUMBER: 60/231,212 PRIOR FILING DATE: 2000-99-08 NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin version 3.0 SEQ ID NO 4 LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
APPLICANT: W. Hua
APPLICANT: Dalton, Willian
TITILE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
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100.0%; Pred. No. 4.2e-52;
iive 0; Mismatches 0;
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                                      Sequence 4, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 100.0
Matches 96; Conservative
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ORGANISM: Homo Sapiens
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                 US-10-380-020-4
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US-10-380-020-2
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100.0%; Score 494; I
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                                                                                                                                                                      HYPOTHETICAL: NO SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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OTHER INFORMATION:
                                                                      LENGTH: 770 amino acids
                                                                                       TYPE: amino acid
STRANDEDNESS: single
                           INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS
                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
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Matches 96; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/045,792
PILING DATE: 19-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 494; DB 11; 100.0%; Pred. No. 4.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Jackson Eq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moarefi, Ismail
Darnell, Jr., James E.
Kuriyan, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/10045792
Publication No. US20030003563A1
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
                                                                                                                                                                                                                                                                                                              LENGTH: 770 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100. Matches 96; Conservative
                                                                                                                                                                                                                                                    TELEX: 133521
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                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-876-773-12
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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
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                                                                                                                       1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
                                                                                                                                                                                                                                                                                                                                                                                                        US-10-038-010-56
; Sequence 56, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; TITLE OF INVENTION: Protein protein interactions in adipocyte cells
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; TITLE OF INVENTION: BA76A;
; CURRENT FILING DATE: 2002-07-23
; PRIOR PPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SEQ ID NO 56
; LENGTH: 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                             Gaps
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   Length 770;
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Publication No. US2030166854A1
GENERAL INFORMATION:
APPLICANT: SERLUDI-CRESCENZI, Ottaviano
APPLICANT: DELLA PIETRA, Linda
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
FILE REPERRNCE: SERLUPI=2
CURRENT APPLICATION NUMBER: US/10/117,087
, DB 14;
4.2e-52;
                                                                                                                                                                                                                                                                              342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 494; DB 14; 100.0%; Pred. No. 4.2e-52;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                           LENGTH: 770 amino acids TYPE: amino acid
      SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino ac
                                                                  TOPOLOGY: linear
                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-925-302-780
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                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
; Wen, Zilong
Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
sequences AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                         Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIE: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DARE: US/10/639,617
FILING DATE: 12-Aug-2003
                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                         ; Score 494; DB 14;
; Pred. No. 4.2e-52;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                                                                                                                                                                                                                                                                                                                                                      61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-073 CIPTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MR-1994
PFILING DATE: 11-MR-1994
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MR-1993
FILING DATE: 19-MR-1993
FILING DATE: 24-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US/09/526,542
PRIOR FILING DATE: 2000-03-19
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 96; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                            TYPE: PRT
ORGANISM: Human
                                                                                                    SEQ ID NO 2
LENGTH: 770
                                                                                                                                                                                   US-10-117-087-2
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282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 341
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                                                                                                         1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNIAMKSAFVVERQPCMPMHPDRPLVIKT 60
                                                        Gaps
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  Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 780, Application US/09925302

Sequence 780, Application US/09925302

Patent No. US20020044941A1

GENERAL INFORMATION:

APPLICANT: ROSen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA104

CURRENT FAPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 780, Application US/09925302
| Bublication No. US20030064072A9
| GENERAL INPORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PA104
| CURRENT APPLICATION NUMBER: US/09/925,302
| CURRENT APPLICATION NUMBER: COO.03-08
| PRIOR APPLICATION NUMBER: PCT/US00/05918
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1909-03-12
| NUMBER OF SEQ ID NOS: 896
| SOFTWARE: PatentIN Ver. 2.0
| SEQ ID NO 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 793;
                                                   Indels
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                                                                                                                                                                                                                                                  GVOFTTKVRLLVKFPELNYOLKIKVCIDKDSGDVAA 400
100.0%; Score 494; DB 17; 100.0%; Pred. No. 4.2e-52;
                                                                                                                                                                                                                     61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Query Match 100.0%; Score 494; DB 10; Length 793; Best Local Similarity 100.0%; Pred. No. 4.3e-52; Matches 96; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                               ; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780
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0; Gaps

Search completed: May 25, 2005, 18:21:52 Job time: 43.375 secs.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 25, 2005, 17:24:07; Search time 9.0566 Seconds Run on:

(without alignments) 1019.898 Million cell updates/sec

Title:

US-10-090-185-25 494 1 KKLEELQQKVSYKGDPIVQH......LNYQLKIKVCIDKDSGDVAA 96 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries Match 100% Maximum

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de			SUMMERIES	
Result		Query				
No.	Score	Match	Length	8	ai .	Description
1	494	100.0	770	7	149508	ISGF3 p91-related
7	489	99.0	770	7	A54444	DNA-binding protei
m	310	62.8	739	0	A46159	interferon-depende
4	283	57.3	748	~	A56047	gamma-interferon a
2	204	41.3	851	~	A46160	interferon alpha-i
9	ö	18.3	848	~	A54740	interleukin-4-indu
7	86.5	17.5	786	~	149274	mammary gland fact
8	Ġ	17.5	793	7	S54772 ·	mammary gland fact
6	ė.	17.5	794	~	G02317	transcription acti
10	86.5	17.5	794	7	S55527	mammary gland fact
11	83.5	16.9	837	~	157557	DNA-Binding Protei
12	72	14.6	393	N	S32458	4-hydroxyphenylpyr
13	72	14.6	393	7	S32821	4-hydroxyphenylpyr
14	7.1	14.4	498	~	T06667	argininosuccinate
15	68	13.8	363	0	S48483	MRS1 protein - yea
16	68	13.8	590	7	A48461	ovarian abundant m
17	68	13.8	1152	7	E71667	2-acylglycerophosp
18	67	٠	376	7	S32820	alloantigen F - ra
19	67	•	402	~	T29703	hypothetical prote
20	67	13.6	415	~	JC7167	C kinase 1 interac
21	67	13.6	508	~	AF1479	fatty-acid-CoA lig
22	99	13.4	376	~	A60236	F protein - mouse
	99	13.4	393	0	T25063	hypothetical prote
24	9	13.4	508	~	AC1119	fatty-acid-CoA lig
25	65.5	13.3	748	~	T47250	complex I intermed
56		13.3	926	۲3	T39082	hypothetical prote
27	64	13.0	334	Н	DEBYMM	malate dehydrogena
28	64	13.0	364	~	T30084	hypothetical prote
29	64	13.0	460	N	H89907	hypothetical prote

translation elonga	perinuclear bindin	probable gtpase ac	meiotic recombinat	mevalonate kinase	dynamin-related pr	ribonucleoside red	beta-lactamase (EC	conserved hypothet	hypothetical prote	probable ABC trans	GAP-associated pro	hypothetical prote	60S RIBOSOMAL PROT	pre-B cell enhanci	proteinase, probab
T43892	A56486	T39954	T41126	S42088	T39373	B84389	PNBSL	A99345	T21556	C71182	A38218	B70042	T48076	873433	B81056
~	~	7	7	н	~	7	-	7	7	7	~	7	7	0	7
395	416	695	339	378	781	804	307	328	369	580	1493	191	256	451	451
12.9	12.8	12.8	12.7	12.7	12.7	12.7	12.6	12.6	12.6	12.6	12.6	12.4	12.4	12.4	12.4
63.5	63	63	62.5	62.5	62.5	62.5	62	62	62	62	62	61.5	61.5	61.5	61.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 09-Uul-2004
C;Accession: 149509
B;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRP, a novel IFN-stimulated gene factor 3 p91-related tr A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: 149508
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
p91-related transcription factor - mouse
```

A;Gene: APRF C;Superfamily: human signal transducer and transcription activator STATSA

Gaps ö Length 770; Indels 100.0%; Score 494; DB 2; ilarity 100.0%; Pred. No. 4.6e-46; Conservative 0; Mismatches 0; Local Similarity nes 96; Conservat Query Match Best Loc Matches

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1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT

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RESULT 2

A5444 DNA-binding protein APRF - human C;Species: Homo sapiens (man) C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004 C;Accession: A54444 C;Accession: A54444 Cell 77, 63-71, 1994 A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr A;Reference number: A54444; MUID:94208062; PMID:7512451

A; Accession: A54444

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C;Species: Homo sapiens (man)
C;Date: 28-OCT-1994 #sequence_revision 28-OCT-1994 #text_change 09-Jul-2004
C;Accession: A54740
C;Accession: A54740
R;Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interleukin-4-induced transcription factor stat - human
                                   57.3%;
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                                                                                                              53; Conservative
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                                                                          Best Local Similarity
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                                       Query Match
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A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in ea A;Reference number: A56047; MUID:94277038; PMID:8007943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-748 <YAM>
A;Residues: 1-748 <YAM>
COOSTANTEROR: PROPER BY GR: U09351; NID: GS09502; PIDN: AAA19692.1; PID: GS09503 C;Superfamily: human signal transducer and transcription activator STATSA C;Keywords: DNA binding; phosphoprotein
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R;Schindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa A;Reference number: A46159; MUID:9236557; PMID:1502203
A;Accession: A46159
A;A
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C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
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Jate: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                        A, Cross-references: GDB:358950
A, Map position: 17421-17421
C;Superfemily: human signal transducer and transcription activator STATSA
C;Keywords: DNA binding; transcription factor
                                                                                                              A;Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 770;
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 489; DB 2;
Pred. No. 1.6e-45;
0; Mismatches 1;
preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 58; Conserv
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Best Local Similarity
                                                                          A; Residues: 1-770 < RES>
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C; Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C; Accession: 446160; S1983; S1894, T; Achersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A; Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator A; Reference number: A46160; MUID:92366558; PMID:1502204
A; Accession: A46160
A; Ascession: A46160
A; Ascession: A46160
A; Molecule type: mRNA; protein
A; Residues: 1-851 <FUL>
A; Cross-references: UNIPPOT:P55830
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A,Residues: 1-651, TXAN-
A)Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; PID:g1293920
R,Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; PID:g1293920
R,Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
Nucleic Acids Res. 23, 459-463, 1995
A,Fitle: The genomic structure of the STAT genes: multiple exons in coincider
A,Reference number: S53873; MUID:95192056; PMID:7885841
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44.4%; Pred. No. 3.3e-14;
tive 19; Mismatches 31; Indels
   Length 748;
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Score 283; DB 2;
Pred. No. 6.1e-23;
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337 GSKFTVRTRLLVRLQEGNESLTVEVSIDRN 366
                                                                     15; Mismatches
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A;Cross-references: EMBL:U18671
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NyAlternate names: stat5 protein
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54772; 149273
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
BMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleuki
A;Reference number: S54772; MulD:95237198; PMID:7720707
                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:Z48538; NID:g758633; PIDN:CAAB R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L. Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
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C;Superfamily: human signal transducer and transcription activator STAT5A
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C;Date: 21-Dec-1996 #Bequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
R;Lin, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: U21103; NID: 9747971; PIDN: AAA80590.1; PID: 9747972
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                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-793 <MUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 86.5; DB 2;
; Pred. No. 0.23;
15; Mismatches 26;
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Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Regidues: 1-793 <RES>
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A;Reference number: H01043
A;Accession: 602317
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-794 <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: Stat5a
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A;Residues: 1-432, E', 434-786 <MUI>
A;Cross-references: BMEL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
A;Cross-references: BMEL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
B;Azam, M.; Brdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,
EMBO J. 14, 1402-1411, 1995
A;Title: Interleukin-3 signals through multiple isoforms of Stat5.
A;Reference number: S54725; MUID:95246733; PMID:7537213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NyAlternate names: STATE protein homolog p80
C;Species: Mus musculus (house mouse)
C;Date: 02-0ul-1996 #sequence revision 02-0ul-1996 #text_change 09-Jul-2004
C;Accession: 149274; SS4773; SS4727
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
R;Liu: Cloning and expression of Stats and an additional homologue (Stat5b) involved
A;Reference number: 149273; WUID:96004632; PMID:7568026
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                                                                            A;Accession: A54740
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-848 <HOU>
A;Cross-references: UMIPROT:P42226
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Gene: Stat5b
C;Superfamily: human signal transducer and transcription activator STAT5A
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Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
                                                                                                                                                                                                                                                                                                        Length 848;
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                                                                                                                                                                                                                                                                                                     18.3%; Score 90.5; DB 2; Length 8 36.2%; Pred. No. 0.091; cive 12; Mismatches 23; Indels
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A;Molecule type: mRNA
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A;Residues: 1-432,'E',434-786 <AZA>
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Best Local Similarity 36.2%
Matches 25; Conservative
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A,Molecule type: protein
A;Residues: 83-118;151-174;194-196;198-224;230-254;256-265;267-273;341-356;358-361;370-
A;Residues: 83-118;151-174;194-196;198-224;230-254;256-265;267-273;341-356;358-361;370-
R;Endo, F.; Awata, H.; Tanoue, A.; Ishiguro, M.; Eda, Y.; Titani, K.; Matsuda, I.
submitted to the EMBL Data Library, October 1992
A;Description: Primary structure deduced from complementary DNA sequence and expression:
A;Reference number: S35889
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A,Residues: 1-120, 'EVCCAADVRGHHTPLDRARQVWBG',145-150, 'TFCLDSR',158,'QPSQTLLHRL',169-393|
A,Residues: 1-120,'EVCCAADVRGHHTPLDRARQVWBG',145-150,'TFCLDSR',158,'QPSQTLLHRL',169-393|
A,Cross-references: EMBL:D13390, NID:g217691; PIDN:BAA02660.1; PID:g217692
C,Superfamily: 4-hydroxyphenylpyruvate_dioxygenase
C,Reywords: homodimer; oxidoreductase
C;Species: Homo sapiens (man)
C;Date: 28-May-1993 #sequence_revision 02-Jun-1994 #text_change 12-Jul-2004
C;Date: 28-May-1993 #sequence_revision 02-Jun-1994 #text_change 12-Jul-2004
C;Accession: 333458; 840298; S31153
R;Rueetschi, U.; Dellsen, A.; Sahlin, P.; Stenman, G.; Rymo, L.; Lindstedt, S.
Eur. J. Biochem. 213, 1081-1089, 1993
A;Title: Human 4-hydroxyphenylpyruvate dioxygenase. Primary structure and chromosomal 1
A;Reference number: S32458; MUID:93279307; PMID:8504803
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 2-23;41-76;82-108;119-142;151-162;167-179;181-217;221-268;271-300;302-310;3
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1993 #text_change 12-Jul-2004
C;Date: 31-Dec-1993 #text_change 12-Jul-2004
C;Accession: S22821; S35880; S35880
B;Endo, F; Awata, H; Tanoue, A.; Ishiguro, M.; Eda, Y.; Titani, K.; Matsuda, J. Biol. Chem. 267, 24235-24240, 1992
A;Title: Primary structure deduced from complementary DNA sequence and expressionical subunits homologous to rat liver-specific alloantigen F.
A;Reference number: S32821; MUID:93077502; PMID:1339442
                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P12754; EMBL:X72389; NID:g288104; PIDN:CAA51082.1; A;Note: the authors did not translate the codon for residue 1 A;Accession: S40298
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C,Superfamily: 4-hydroxyphenylpyruvate_dioxygenase
C,Keywords: homodimer; oxidoreductase
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Best Local Similarity 24.4%; Pred. NO. 7,
Watches 22; Conservative 17; Mismatches
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A; Residues: 1-393 < END1>
                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-393 <RU1>
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                                                                                                                                                                                                                                  the cytokine regula
                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-794 <WAK.>
A; Residues: 1-794 <WAK.>
A; Cross-references: UNIPROT: P42231; EMBL: X78428; NID: 9602354; PIDN: CAA55191.1; PID: 96023
A; Note: this is a revision to the sequence from reference $44353
EMBO J. 13, 2182-2191, 1994
A; Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcri
A; Reference number: $44353; MUID: 94244619; PMID: 7514531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWA-Binding Protein and transcription factor - mouse (5) Species: Mus musculus (house mouse) (2) Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004 (5) Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004 (5) Accession: 157557 (6) Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Cleve Mol. Cell. Biol. 15, 3336-3343, 1995 (7) Aritle: Cloning of murine State and human State, State proteins that are tyrosine phosph A. Reference number: 157557; MUID:95280394; PMID:7760829 (7) A. A. Accession: 157557
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                                    mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Dacte: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S5527; 844353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cyt
A;Reference number: S55527; MUID:95188889; PMID:7882987
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A;Gene: STAT6
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: this sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A
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33.3%; Pred. No. 0.52;
iive 15; Mismatches
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FOAGVRFLL 297
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Matches 23; Conserv
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Best Local S
Matches 22
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KVSYKGDPIV-----QHRPMLEERIVELF-RNLMKSAFVVERQPCMPMHPDRPLVIKT 60
                                                                                                                                                270 PILSST----TGLNFSLKDCLSLDTGKDASDM 297
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submitted to the EMBL Data Library, October 1994

A, Reference number: $48478

A, Molecule type: DNA

A, Molecule type: DNA

A, Residues: 1-363 - (ROW)

A, Cross-references: UNIPROT: P07266; GB: Z47047; EMBL: Z38061; NID: g603997; PID: g763366; MI

R, Kreike, J.; Schulze, M.; Ahne, F.; Lang, B.F.

EMBO J. 6, 2123-2129, 1987

A, Title: A yeast nuclear gene, MRS1, involved in mitochondrial RNA splicing: nucleotide

A, Reference number: A91075; MUID: 88004424; PMID: 2443348
                                                                                                                                                                                                                                                                                                           De
                                                                                                                                                                                                                                                              C;Accession: T06667
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; Cheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller, C. aubmitted to the Protein Sequence Database, April 1999
A;Accession: T06667
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                                                                                                                                                           argininosuccinate synthase (EC 6.3.4.5) - Arabidopsis thaliana N;Alternate names: protein F617.40 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #sequence_revision 23-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRS1 protein - yeast (Saccharomyces cerevisiae)
NiAlternate names: protein YIRO21w
Cispecies: Saccharomyces cerevisiae
Cispecies: 02-Dec.1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
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A; Residues: 1-181, 'P'. 183-317,'A', 319-363 < KRE>
A; Croser-references: EMBL:X05509; NID:g3987; PIDN:CAA29053.1; PID:g3988
C; Genetics:
A; Gene: SGD:MRS1; PET157
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A;Experimental source: cultivar Columbia; BAC clone F617
GGenetics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Map position: 4
A;Map position: 4
A;Introns: 25/1; 100/1; 146/2; 162/3; 223/3; 285/3; 315/2
C;Superfamily: argininosuccinate synthase
C;Keywords: ligase
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306 AKIRVKESIDVLEELKILVDYDEKGYLLQI 335
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Matches 21; Conservative
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A,Genome: nuclear
C,Keywords: mitochondrion
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A; Residues: 1-498 <BEV>
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1 KKLEELQQKVSYKGDPIVQH......LNYQLKIKVCIDKDSGDVAA
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1612378 seqs, 512079187 residues
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STA3_HUMAN
STA3_MOUSE
STA3_RAT
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STA1_HUMAN
Q68D00
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Q7zz77
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STA4 HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO: 0005634; C: nucleus; IEA.

GO; GO: 0005634; C: nucleus; IEA.

GO; GO: 0004871; F: signal transducer activity; IEA.

GO; GO: 0003700; F: transcription factor activity; IEA.

GO; GO: 0007165; P: regulation of transcription, DNA-dependent; IEA.

GO; GO: 0007165; P: signal transduction; IEA.

InterPro; IPR001217; STAT.

InterPro; IPR001217; STAT.

Pfam; PF02104; STAT. bind; 1.
                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
NCBI_TaxID=9544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 163;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Signal transducer and activator of transcription (Fragment)
Name-STAT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 494; DB 2; Length 1
100.0%; Pred. No. 1.3e-46;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                              Arredondo J.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF227560; AAF73401.1; -.
HSSP; P42227; 1BG1...7... TEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;
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C STA3 BOVIN

AC P6163;

DT 05-UUL-2004 (Rel. 44, Last sequence update)

DT 25-UUL-2004 (Rel. 45, Last annotation update)

DT 25-CVT-2004 (Rel. 45, Last annotation update)

E Signal transducer and activator of transcription 3.
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                                                                                                                                                       Macaca mulatta (Rhesus macaque).
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complexes."
                                          oathway
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                     TISSUE-Mammary gland;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
Turb STATBS-encoding gene was flipped across the STATB/STATSA-locus during ruminant evolution.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6) responsive elements identified in the promoters of various acute-phase protein genes (By similarity).
-!- PATHWAY: Involved in the gpl30-mediated signaling pathway.
-!- STBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).
-!- SIMILARITY: Belongs to the transcription factor STAT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNIMKSAFVVERQPCMPMHPDRPLVIKT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KKLEELQQKVSYKGDPIVQHRPMLERRIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphotyrosine (by JAK) (By similarity). Phosphoserine (By similarity). 9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50001; SH2; 1. Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STA3 HUMAN STANDARD; PRT; 770 AA.
P40763; 014916; Q9BW54;
01-FRE-1995 (Rel. 31, Created)
05-JUL-2004 (Rel. 4F). Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 494; DB 1;
Pred. No. 7.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ620655; CAF06182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                770 AA; 87974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               response factor).
Name=STAT3; Synonyms=APRF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similaricy
nes 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Name=STAT3;
Bos taurus (Bovine)
                                                                                              SEQUENCE FROM N.A.
                                                                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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TISSUEEKidney, and Pancreas;

(TISSUEEKidney, and Pancreas;

(MEDINRE-228825; PubMede=12477932; DOI=10.1073/pnas.242603899;

(MEDINRE-228825; PubMede=12477932; MEDING C.M., Schuler G.D., Alacher C.F., Bhat N.K., Alacher C.F., Bhat N.K., Alacher C.F., Bhat N.K., Alacher C.F., Branger C.M., Stapleton M.J., McGrana R.J., Malek J.A., Abramson R.D., Mullahy S.J., McGwan P.J., McGrana R.J., Lu X., Gibbs R.A., Alacher C.F., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Alacher C.F., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Abrare M.A., Schein J.B., Joseph J., Marra M.A.,
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J. B101. Chem. 277:8064-8011(2002).

-I. FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOA1.
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
-!- ALTERNATIVE PRODUCTS:
Yoshida K., Sudo T., Naruto M., Kishimoto T.; "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOPORM DEL-701), AND VARIANT ILE-143.
Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
Rajkumar N., Yi Q., Nickerson D.A.;
"SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
"Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
"Highly conserved amino-acid sequence between murine STAT3 and a revised human STAT3 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-NOV-1995
                                                                                                                          STA3 MOUSE
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                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphotyrosine (by JAK) (By similarity).
                    ISOId=P40763-2; Sequence=VSP 010474;
-!- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.
-!- FTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIP, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.
-!- SIMILARITY: Balongs to the transcription factor STAT family.
-!- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing; DNA-binding; Nuclear protein; ation; Polymorphism; SH2 domain; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                   :
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 494; DB 1; Length 770; Best Local Similarity 100.0%; Pred. No. 7.7e-46; Matches 96; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphoserine (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F -> Y (in Ref. 1).
V -> L (in Ref. 1).
T -> A (in Ref. 1).
GC00632211C8012D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q -> K (in dbSNP:1803125)
/FTId=VAR_018683.
M -> I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (in Ref. 1).
IsoId=P40763-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                            EMBL, AJ012463; CRA1032 1; EMBL, AY572796; AAS66986.1; EMBL; BC000627; AAH00627.1; EMBL; BC014482; AAH14482.1; PIR; AF029311; AAB84254.1; PIR; A54444; A54444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activator, Alternative splicing
Phosphorylation, Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PP00017; SH2; 1.
Pfam; PP01017; STAT alpha; 1.
Pfam; PP02864; STAT bind; 1.
Pfam; PP02865; STAT int; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88067 MW;
                                                                                                                                                                                                                                                   EMBL; L29277; AAA58374.1; -.
                                                                                                                                                                                                                                                                                                                                                      TRANSFAC; T01493; -.
Genew; HGNC:11364; STAT3.
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667 6
730 7
           Name=Del-701
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SEQUENCE
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"Acute phase response factor and additional members of the interferon-
stimulated gene factor 3 family integrate diverse signals from
cytokines, interferons, and growth factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAINBALB/C; TISSUE-Liver;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
Yoshida K., Sudo T., Naruto M., Kishimoto T.;
"Molecular cloning of ARRF, a novel IRN-stimulated gene factor 3 p91-
related, transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Thymus;
MEDLINE=94188718; PubMed=8140422;
Zhong Z., Wen Z., Darnell J.E. Jr.;
"Stat3: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6.";
Science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and C57BL/6; TISSUB=Liver;
MEDLINE=96016116; PubMed=7568080;
Schaefer T.S., Sanders L.K., Nathans D.;
"Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM STAT3A).
STRAIN=C57BL/6J, and NOD/LtJ;
Bavodoi-Semiromi A., She J.-X.;
"A mutant Stat5b with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase response factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pubmed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.;
                                                                                       GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 377
                                                       96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995)
                                                       GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA
                                                                                                                                                                                                                  (Rel. 32, Created)
(Rel. 34, Last sequence update)
(Rel. 45, Last annotation update)
                                                                                                                                                                                    770 AA
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MEDLINE=95014185; PubMed=7523373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raz R., Durbin J.E., Levy D.E.;
                                                                                                                                                                                                                                                                                                                 Name=Stat3; Synonyms=Aprf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zebrafish to mouse.";
Genomics 71:150-155(2001).
                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sell 77:63-71(1994).
                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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Gaps

0;

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                                                             SECURATE FURNA N.A. (120/CRW SIA11A).

SECURATINE-EVBAN TISSUE-Mammary gland;
MEDLINE-22388257; PubMed=12477332; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heith F.,
B topleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B Raha S.S., Loquelilano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
B lakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
B Butterfield Y.S.N., Krzywinski M.I., Schlaka U., Smallus D.E.,
B chnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

""" "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 394:145-151(1998).

-!- FUNCTION: Transcription factor that binds to the interleukin-6

-!- FUNCTION: Transcription factor that binds to the interleukin-6

(IL-6)-responsive elements identified in the promoters of various acute-phase protein genes. STAT3B interacts with the N-terminal part of JUN to activate such promoters in a cooperative way.

-!- PATHWAY: Involved in the gpl30-mediated signaling pathway.

-!- FUNCTIONITY: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.

-!- ALTERNATIVE PRODUCTS:

-!- ALTERNATIVE PRODUCTS:

--- SUBCELLULAR LOCATION: Named isoforms=3;

Name=Stat3A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.
MEDLINE-95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
Men Z., Zhong Z., Darnell J.E. Jr.;
Maximal activation of transcription by Statl and Stat3 requires both
tyrosine and serine phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isold=P4227-3; Sequence=VSP 010475;
ISOLG=P4227-3; Sequence=VSP 010475;
TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and kidney. STAT3B is also detected in the liver, although in a much less abundant manner.

PTH: Yycosine phosphorylated in response to IL-6, IL-11, CNTF, ILF, CSF-1, EGF, PDGF, IFN-alpha and OSM Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity (By similarity). SIMILARITY: Belongs to the transcription factor STAT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
MEDLLINE=9833477; PubMed=9671289; DOI=10.1038/28101;
Becker S., Groner B., Mueller C.W.;
"Three-dimensional structure of the Stat3beta homodimer bound to
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P42227-2; Sequence=VSP_006287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P42227-1; Sequence=Displayed;
                                                  SEQUENCE FROM N.A. (ISOFORM STAT3A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 82:241-250(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Del-701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Stat3B;
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FDMDLTSECATSPM -> FIDAVWK (in isoform
Stat3B).
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            EMBL; 129278; AAA19422.1; ---

REMBL; 106922; AAA19422.1; ---

REMBL; 106922; AAA19422.1; ---

REMBL; 108709; AAC52612.1; ---

REMBL; AR246978; AAA56668.1; ---

REMBL; AR294989; AAA75418.1; ---

REMBL; AX299489; AAA75418.1; ---

REMBL; AX299489; AAA75418.1; ---

REMBL; AX299489; AAA75418.1; ---

REMBL; AX299489; AAA77418.1; ---

REMBL; AXA77418.1; ---

REMBL; AXA77419.1; ---

REMBL; AXA77410.1; ARA7 bind; 1.

REMBL; REMBL; REMBL; ACTIVATOR; ACTIVATOR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (In isoform Del-701).
/FTId=VSP_010475.
S->A: Decreased transcriptional
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S -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal transducer and activator of transcription 3. Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2004) F.C.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: AV641397; Ad764897.1;
EMBL: AV641397; Ad764897.1;
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:00073700; F:transcription factor activity; IEA.
GO; GO:0007342; P:intraecription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000990; SH3.
InterPro; IPR001217; STAT.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia, Anura; Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Last annotation update)
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                                                                                                                                                     GVOPTTKVRLLVKFPBLNYQLKIKVCIDKDSGDVAA
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Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28.
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                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibsib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Transcription factors Stat3 and Stat5b are present in rat liver nuclei late in an acute phase response and bind interleukin-6 response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphotyrosine (by JAK) (By similarity). Phosphoserine (By similarity). D74A0C76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 270:29998-30006(1995).
-!- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
770 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR008967; P53 like_DNA_bnd
InterPro; IPR000980; SH2.
                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              770 AA; 88039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X91810; CAA62920.1; -. HSSP; P42227; 1BG1.
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Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                       Name=Stat3;
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Length 771;

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A Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;

Bubbi, AJ620661; CaF061881; F.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.

R GO; GO:0007165; P:segulation of transcription, DNA-dependent; IEA.

R GO; GO:0007165; P:segulation of transcription, DNA-dependent; IEA.

InterPro; IPR00157; F33 like_DNA_bnd.

InterPro; IPR001217; STAT.

IN Pfam; PF02864; STAT_alpha; 1.

R Pfam; PF02864; STAT_alpha; 1.
                                                                                                                                                                   R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:0004871; F:signal transducer activity; IEA.
R GO; GO:0007242; P:intracellular signaling cascade; IEA.
R GO; GO:0007242; P:intracellular signaling cascade; IEA.
R GO; GO:0007242; P:intracellular signaling cascade; IEA.
R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
R InterPro; IPR000980; SH2.
R InterPro; IPR000980; SH2.
R Pfam; PF00017; SH2.
R Pfam; PF00017; SH2.
R Pfam; PF00017; SH2 ll.
R Pfam; PF00017; SH2 ll.
R Pfam; PF00018; SH2.
R Pfam; PF00052; SH2; 1.
R PMART; SM00252; SH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Asashima M., Yokota T.,
Asashima M., Yokota T.,
"Activation of Stat3 by cytokine receptor gpl30 ventralizes Xenopus embryos independent of BMP-4.",
EMBL; AB017701; BAA86061.1; -.
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Mammary gland;
Modenaar A., Wheeler T.T., McCracken J.Y., Seyfert H.M.;
"The STAT3-encoding gene resides within the 40 kbp gap between the STAT5- and STAT5B-encoding gene in cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-stat3;
Das taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 and activator of transcription 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.0%; Score 489; DB 2; Length 769; 99.0%; Pred. No. 2.8e-45; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50001; SH2; 1.
769 AA; 87974 MW; 0905C03263303069 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
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hes 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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TISSUE=Embryo;

X Structus From M.T.

X Structus From S. W. Grouse L.H., Derge J.G.,

X Structusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Structusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Alausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

X Alausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Workernan K.J., Marewon R.D., Mullahy S.J.,

R Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Helton E., Ketteman M., Madan A., Youchman J.W., Green E.D., Dickson M.C.,

Rh Mitting M., Madan A., Youchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                    1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                                                                      16 KKLEGLQQKVSYKGDPIVQHRPMLEBRIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
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0
                                                                                       98.6%; Score 487; DB 2; Length 161; 99.0%; Pred. No. 7.7e-46; ive 0; Mismatches 1; Indels
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18342 MW; SDCEE8F2C3A48191 CRC64;
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GO: GO:0004871; F:signal transducer activity; IEA.
GO: GO:0003700; F:transcription factor activity; IEA.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                              95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
   161 1
161 AA;
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                                                                                           Query Match
Best Local Similarity
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RESULT 11
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WE Strausberg R.D.; Feingold E.A.; Grouse L.H.; Derge J.G.;

WA Klausner R.D.; Collins F.S.; Wagner L.; Shemmen C.M.; Schuler G.D.;

A Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

A Altschul S.F.; Jecherg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

A Diatchenko L.; Marusina K., Farmer A.A.; Rubin G.M.; Hong L.;

A Brownstein M.J.; Ubdin T.B.; Toshiyuki S., Carninoi P., Prange C.;

A Brownstein M.J.; Ubdin T.B.; Toshiyuki S., Carninoi P., Prange C.;

A Brownstein M.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

A Rodards S.W. Worley D.M.; Sodergen B.J.; Lu X.; Gibbs R.A.; Hulyk S.W.;

A Villalon D.K.; Murny D.M.; Sodergren B.J.; Lu X.; Gibbs R.A.; Hulyk S.W.;

A Willian A.; Youchman J.W.; Green B.D.; Dickson M.C.;

RA Blakesley R.W.; Touchman J.W.; Green B.D.; Dickson M.C.;

RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;

A Rayminki M.I.; Skalska U.; Smallus D.E.; Schnerch A.; Schein J.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNIMKSAFVVERQPCMPMHPDRPLVIKT
                                                                                                                                                                                                                                                                                                                                                         Gaps
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; PS3_like_DNA_bnd.
InterPro; IPR009867; PS4Z.
InterPro; IPR001217; STAT.
InterPro; IPR001217; STAT.
Pfam; PP001017; STAT_alpha; 1.
Pfam; PP01017; STAT_alpha; 1.
Pfam; PP02864; STAT_bnd; 1.
SMART; SM00252; STAT_int; 1.
SWART; RS0001; SH2; 1.
SRQUENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;
                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                       96.2%; Score 475; DB 2; Length 766; 95.8%; Pred. No. 9.7e-44; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
Strauberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC045276; AAH45276.1; --
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Danio rerio).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0005634; C:nucleus; IEA.
                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyprinidae; Danio.
NCBI TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Q7ZTS5;
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MEDINES-2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINES-2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINES-2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINES-2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINES-2188257; PubMed=124.7932; DOI=10.1073/pnas.242603899;

MEDINES R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

MEDINES R.D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MEDINES S., Loquellano M.S., Poshiyuki S., Carninori P., Parange C.,

MEDINES S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MEDINES S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Miling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Maring M., Madan A., Young A.C., Shevchenko Y., Sohein J.E.,

A Dones S.J., Marra M.A.;

Magneration and initial analysis of more than 15,000 full-length human

Man mouse CDNA sequences.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008967; FS3 like_DNA_bnd.
InterPro; IPR001217; STAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                          96.0%; Score 474; DB 2; Length 41 93.8%; Pred. No. 6.2e-44; ive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BCG 12 1;
ZFIN; ZDB-GENE-980556-68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0001700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                         Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
SEQUENCE 414 AA; 48253 MW; 0FFD1B509B7526BD CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAA 96
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.8'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyprinidae; Danio.
NCBI_TaxID=7955;
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SEQUENCE
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                            RESULT 13
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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EMBL; AJ005693; CAA06677.1; -.

EMBL; AJ005693; CAA06677.1; -.

ZEIN; ZDB-GENE-980526-68; stat3.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:000471; F:signal transducer activity; IEA.

GO; GO:000471; F:signal transducer activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000980; SH12.
transcription, DNA-dependent; IEA
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                                                                                                                                                                                                                                                                                                                                                                      Length 786;
                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                         90039 MW; FC7371D0B0E5447E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 GVQFTTKVRLLVKFPELNYQLKIKVCIDKESGDVAA 378
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                                                                                                                                                                                                                                                                                                                                                                         96.0%; Score 474; DB 2;
93.8%; Pred. No. 1.3e-43;
live 5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio).
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                            InterPro; IPR008967; P53_like_DNA_bnd
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
P:regulation of
                                                                                                                             Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 786 AA; 90039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
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SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 806 AA; 92151 M
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GO; GO:0006355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=stat3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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283 KKLEELQQKVSYKGDPIIQHRPALEEKIVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKT 342
                                                                                                                                                                                                                                                                                                                                                                                       Liu R., Hong Y.;
Submitted (MAY-2004) to the EWEL/GenBank/DDBJ databases.
Submitted (MAY-2004) to the EWEL/GenBank/DDBJ databases.
RM 2050:0005634; C:nucleus; IEA.
GO; GO:00004871; F:signal transducer activity; IEA.
RO; GO:0003700; F:transcription factor activity; IEA.
RO; GO:0000322; P:intraccllular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
R O; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR0098967; F83_like_DNA_bnd.
InterPro; IPR0017; STAT.
R Pfam; PF00017; STAT.
R Pfam; PF00017; STAT alpha; 1.
R Pfam; PF008665; STAT_bnd; 1.
R PROSTER: PS00001; STAT_lnt; 1.
R PROSTER: PS00001; STAT_lnt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT
25-OCT-2004 (TrEWBLrel. 28, Created)
25-OCT-2004 (TrEWBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Signal transducer and activation of transcription factor 3.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Bukaryota: Metazoa: Chordata: Craniata: Vertebrata; Buteleostomi; Actinopterygii; Meopterygii; Teleostei; Suteleostei; Acanthomorpha; Acanthomorpha; Acanthoterygii; Percomorpha; Atherinomorpha; Meoteleostei; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TTEMBLrel. 27, Last sequence update)
05-JUL-2004 (TTEMBLrel. 27, Last annotation update)
05-JUL-2004 (TTEMBLrel. 27, Last annotation update)
Signal transducer and activator of transcription 3 isoform 1.
Oryzias latipse (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008967; P53_like_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.5%; Score 472; DB 2; Length 765; 93.8%; Pred. No. 2.1e-43;
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Submitted (MAX-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY641434; AAT46364.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87566 MW; F5D01408748EC703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 GVQFTNKVRLLVKFPELNYQLKIKVCIDKESGDVAA 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
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Best Local Similarity
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                                                                                                                                                                                                                  1 KKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKT 60
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                                                                                                                                                                                      Gaps
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P4227; 1BG1.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004671; F:signal transducer activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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                                                                                                                                                   Length 785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.3%; Score 461; DB 2; Length 764; 91.7%; Pred. No. 3.5e-42; ive 5; Mismatches 3; Indels
                                                                                                                                                95.5%; Score 472; DB 2; Length 78 93.8%; Pred. No. 2.2e-43; rative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307106; AAL09415.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH2; 1.
; 87411 MW; E661FFE18BEFD8BE CRC64;
                                                                                                                  89643 MW; 81F231BDE27DE938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Q90Y16;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                       343 GVQPTNKVRLLVKFPELNYQLKIKVCIDKESGDVAA 378
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                                                                                                                                                                                                                                                                                                                                                                                                        764 AA
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon fluviatilis (Puffer fish)
                           Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 785 AA; 89643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SMART; SM0252; SH2; 1.
                                                                                                                                                                 Local Similarity 93.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.7'
Matches 88; Conservative
 InterPro; IPR000980; SH2
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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PROSITE; PS50001;
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Search completed: May 25, 2005, 17:43:42 Job time : 40.9444 secs

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Mouse

Human sig Human Sta

Human :

Human

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/note= "Wild type Arg substituted with Ala corresponds to 350 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild type Val substituted with Ala corresponds to 151 position of Stat-3 protein"

    .25
/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"

                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild type Leu substituted with Ala; corresponds
to 148 position of Stat-3 protein"
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild type Lys substituted with Ala corresponds 348 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                               Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                              Mouse Stat3 mutant (L148A, V151A, T346A, K348A, R350A) protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild type Thr substituted with Ala 346 position of Stat-3 protein" Misc-difference 219
                                                                                                                                                                                                 ALIGNMENTS
                 AAY72851
AAY72864
AAY72855
AAY72868
AAY72868
AAY72869
AAY72864
AAY72864
AAY72864
AAY72864
AAY72864
AAW62996
ABU64748
AAW62996
ABU64748
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AAW62995
ABU04747
ABU04735
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                          . AAY72860 standard; protein; 229 AA
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AAY72860;
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Rat Prote
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N-termina
Murine ST
Human bai
                                                          May 25, 2005, 17:14:45; Search time 121.891 Seconds (without alignments) 726.619 Million cell updates/sec
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Abu10476 Adu04365 Adu04365 Adu54789 I
Adb54489 I
Adb5442 I
Add7438 I
Ady72861 N
Aar82993 I
Aab19964 I
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Aay72846
Aay72846
Aar72082
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
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AAE22055
ABB57164
AAE22054
AAE22056
AAR82995
AAY03768
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ADN04365
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AAW03176
AAY72863
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AAR82993
AAB19964
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as; *
geneseqp2003bs; *
geneseqp20048; *
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geneseqp1990s:*
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Post-processing:

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11160 11155 11155 11155 11155 11155 11155 11154 11144 11144

Result 8 1144 1140.5 1139

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Zhang X, Horvath C,
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Best Local Similarity
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                                                       31-AUG-1999;
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08-MAR-2001
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                                                                                                                                       The present sequence is mouse Stat3 mutant protein fragment containing replacing of Stat3 protein. This mutant is obtained by replacing Leu 148 with Ala, Val 151 with Ala, Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comperises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation
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C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse, Stat3 protein, transcription factor; c-Jun, gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .25
/note= "Stat3-c-Jun interaction region 1; corresponds
130-154 position of Stat3 protein"
213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NHPTAAVVTEKQQMLEQHAQDARKRVQDLEQKWKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                     Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                          Score 1160; DB 4; Length 229;
Pred. No. 1.5e-98;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Stat3 protein fragment #8 (130-358 amino acids).
               Darnell JE;
             Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY72850 standard; protein; 229
                                                                                                               Example 4; Page; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                           99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.1
Matches 227; Conservative
             Horvath C,
                                                                                                                                                                                                                                                                                                                                                Sequence 229 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY72850;
                                                                                                                                                                                                                                                                                                                                                                              Query Match
               Zhang X,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is mouse Stat3 protein fragment containing 130-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GINNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                      Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse Stat3 protein fragment #4 (107-358 amino acids).
                                                                                                                                                                                                   Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1155; DB 4;
Pred. No. 4.4e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.9%; Scol. 98.7%; Pred. No. 4... 98.7%; O; Mismatches
                                                                                                                                                                                                   Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 65; Page 76-77; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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30-AUG-2000; 2000WO-US023822.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 98.7
Matches 226; Conservative
                                                                                                                                   (UYRQ ) UNIV ROCKEFELLER
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corresponds to

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GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a method Stat 23, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for transformation. These identifying agents are used in the treatment of Stat protein comprises the N-terminal domain, coiled-coil domain, bund binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                   /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying an agent for use in modulating the interaction between transcription factor c\text{-Jun} and a Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.8%; Score 1155; DB 4; Length 271; 98.7%; Pred. No. 5.5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VELPRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL
                                          interaction region 1;
Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                  Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Wrzeszcynska MH,
                  /note= "Stat3-c-Jun i.
130-154 position of St
236. .252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 65; Page 67-68; 86pp; English.
  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR72082 standard; protein; 770 AA
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                                                                                                                                                                                                                                                                                                                                                                    Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-226705/23
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                                                                                                                                                                WO200116605-A2
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27-SEP-1995
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Region
                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is mouse Stat3 protein fragment containing 107-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of sysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, colled-coil domain, bNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 NHPTAAVVTEKQQMLEQHLKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse, Stat3 protein, transcription factor, c-Jun, gene transcription, cellular transformation, dysproliferative disease, cancer, psoriasis,
  corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1155; DB 4; Length 252;
Pred. No. 5e-98;
0; Mismatches 3; Indels (
/note= "Stat3-c-Jun interaction region 2;
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse Stat3 protein fragment #2 (107-377 amino acids)
                                                                                                                                                                                                                                                                   Darnell JE;
                                                                                                                                                                                                                                                                 Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 65; Page 73; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY72841 standard; protein; 271
                                                                                                                                           30-AUG-2000; 2000WO-US023822
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98.7%;
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                                                                                                                                                                                                                         (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                 Horvath C,
                                                                                                                                                                                                                                                                                                         WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 226; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 252 AA;
                                                             WO200116605-A2
                                                                                                                                                                                 31-AUG-1999;
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                                                                                                     08-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                 Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g. oncogenesis, inflammation, parasitic disease or autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse signal transducer and activator of transcription (STAT) protein STAT4 (AAM01176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery vi DNA binding in a receptor-ligand specific manner. STAT proteins and the DNA binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and activation of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NHPTAAVVTEKOOMLEQHLODVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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  STAT; STAT4; signal transducer and activator of transcription; DNA binding protein; ligand; receptor; oncogenesis; inflammation; autoimmune disease; antagonist; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.8%; Score 1155; DB 2; Length 770; 98.7%; Pred. No. 2.2e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                     198. .508
|label= DNA binding domain
|/note= "Claim 3, page 110"
                                                                                                                                                                                                                                                                                                                                                                                                               Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 87-90; 138pp; English.
                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                             Horvath
                                                                                                                                                                                                                                                                                              95WO-US017025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226; Conservative
                                                                                                                                                                                                                                                                                                                                                                        (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-333941/33.
                                                                                                                                                                                                                                                                                                                                                                                                             Wen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT31280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 770 AA;
                                                                                                                                                                                                                                                                                              28-DEC-1995;
                                                                                                                                                                                                                                                                                                                                    06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                           Darnell JE,
                                                                                                                                                                                                                                                          11-JUL-1996.
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Best Local S
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                                                                                                                      Key
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AC AAY7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 Kna protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339-40) were cloned in plasmids 13sfl and 19sf6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
Signal transducer and activator of transcription; STAT; 19sf6; Stat3; receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKOOMLEQHLODVRKRVODLEQKMKVVENLODDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1155; DB 2; Length 770;
Pred. No. 2.2e-97;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ζ;
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                                                                                                                                                                                                                                                                                                                                                                          Wen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 107-110; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                          Shuai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW03176 standard; protein; 770 AA
                                                                                                                                                                                                                                   93US-00126588.
93US-00126595.
94US-00212184.
94US-00212185.
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98.7%;
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les 226; Conservative
                                                                                                                                                                                                                                                                                                                                    (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-139598/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ89340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 770 AA;
                                                                                                                                                                                                                                   24-SEP-1993;
24-SEP-1993;
11-MAR-1994;
                                                                                                                    WO9508629-A1
                                                                                                                                                                                                 26-SEP-1994;
                                                                                                                                                                                                                                                                                              11-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                          Darnell JE,
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                                                                                                                                                           30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse STAT4
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GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing 130-158 amino acids of Stat3 protein. This mutant is obtained by replacing Leu 148 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type Leu substituted with Ala; corresponds to 148 position of Stat-3 protein"
                                                                                                                                                                                                              Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NHPTAAVVTEKOOMLEQHLODVRKRVODLEQKMKVVENLODDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is mouse Stat3 mutant (L148A) protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                  Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.4%; Score 1150; DB 4; 98.3%; Pred. No. 1.3e-97; ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang X, Horvath C, Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                               AAY72862 standard; protein; 229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 66; Page 85; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2000; 2000WO-US023822.
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                                                                                                                                       (first entry)
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Best Local Similarity 98.3
Matches 225; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                            AAY72862;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is mouse Stat3 mutant (V151A) protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing Val 151 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                          /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
                                                                                                                                                                                                                                                                                             /note= "Wild type Val substituted with Ala corresponds 151 position of Stat-3 protein"
                                   Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psorlasis; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                            213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACIGGPPNICLDRLENWITSLABSQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying an agent for use in modulating the interaction between
Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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Pred. No. 1e-97;
0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Darnell JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                               Location/Qualifiers
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Best Local Similarity 98.3
Matches 225; Conservative
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Length 229;

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us-10-090-185-29.rag

with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, slogren's syndrome, scleroderma, polymyostits, chronic active hepatitis, slogren's syndrome, scleroderma, polymyostits, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating epecific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human stated.

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ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoprais, stroke; angiogenesis; myocardial infarction; hypoplycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; gpilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.
                                                              VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
713. .714
/note= "Encoded by ACA CCA TTC"
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                                                                                                                                     AAE22055 standard; protein; 720 AA
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                                                                                                                                                                                       (first entry)
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(UYSF-) UNIV SOUTH FLORIDA
                                                                                                                                                                                                             Human Stat3beta protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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121
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                                                                                                                                                                                                                                                                                                                   130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                  GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
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                                                                                                                                                                                                                                           97.9%; Score 1144; DB 5; Length 720; 97.8%; Pred. No. 2e-96; ive 1; Mismatches 4; Indels
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N-PSDB; ABI99454.
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                   Sequence 720 AA;
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Best Local &
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, infammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyiai, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy

Modulating anglogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator of transcription 3.

N-PSDB; AAD35066.

Disclosure; Page 87-89; 94pp; English.

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conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
determining the expression profile of a gene group comprising these
                                                                                                                                          present invention describes a method for examining ischaemic
                                                                                  Claim 2; Page 1084-1087; 2690pp; English
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130 NHPTAAVVTEKOOMLEQHLODVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                              120
                                                                                                                                                             249
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                                                                                                                                              190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
                                                                                                                                                                                           121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                             1 NHPTAAVVTEKOOMLEOHLODVRKRVQDLEOKMKVVENLQDDFDFNYKTLKSOGDMQDLN
                                                                                                                              GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
                                Gaps
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                                                                                                                                                                                                                                                                           Score 1144; DB 5; Length 769;
Pred. No. 2.2e-96;
                                  4; Indels
                                1; Mismatches
   97.9%;
Query Match 97.9
Best Local Similarity 97.8
Matches 224; Conservative
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AAE22054 standard; protein; 769 AA. 25-JUL-2002 (first entry) Human Stat3 protein. AAE22054; RESULT 

Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; anapidgenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrestiinsulin dependent diabetes meilitus; emphysema; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative diseorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.

Homo sapiens

WO200220032-A1.

14-MAR-2002

10-SEP-2001; 2001WO-US028254.

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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that condulate the activity of signal transducer and activator of transcription of Stat1). Modulating angiogenesis is useful for treating or preventing thypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia in the lower extremities, infarction, inflammation, trauma, vascular occlusion, prematal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chitogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, considered syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, permicious canemia, autoimmune thyroditis, idiopathic Addison's disease, victuating a strinits, autoimmune thyroditis, idiopathic Addison's disease, victuation preventing or treating chitertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating considers and considered the activity and organic and a succession of an each of a succession of a
                                                                                                                                                                                                                                                                                                                                      Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 83-85; 94pp; English.
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                             08-SEP-2000; 2000US-0231212P
                                                                                                                                                                                     Jove R,
                                                                                       (UYJO ) UNIV JOHNS HOPKINS. (UYSF-) UNIV SOUTH FLORIDA.
                                                                                                                                                                                                                                                  WPI; 2002-362218/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription 3.
                                                                                                                                                                                     Yu H, Pardoll D,
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Sequence 769 AA;

Gaps ö 97.9%; Score 1144; DB 5; Length 769; 97.8%; Pred. No. 2.2e-96; ive 1; Mismatches 4; Indels Best Local Similarity 97.8 Matches 224; Conservative Query Match

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189 130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI **ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI** 61 190 121 셤 ò ઠે 셤 ò 유

VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 181 310

ઠ 용 RESULT 12 AAE22056

AAE22056 standard; protein; 769 П

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Sequence 769 AA;

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AAE22056;

Human protein related to angiogenesis regulation.

immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; anglogenesis; myoardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; emphysema; trauma; scleroderma; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; sprincipitis; polymyositis; theumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion. Human; signal transducer and activator of transcription 3; ischaemia

Homo sapiens.

WO200220032-A1.

14-MAR-2002.

10-SEP-2001; 2001WO-US028254

08-SEP-2000; 2000US-0231212P

(UYJO ) UNIV JOHNS HOPKINS (UYSF-) UNIV SOUTH FLORIDA

Dalton W; Yu H, Pardoll D, Jove R,

WPI; 2002-362218/39.

Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator of transcription 3.

Disclosure; Page 83-85; 94pp; English

The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia in the lower extremities, infarction, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, chronic obstructing a symptom of an autoimmune response is useful for with neovascularisation. Suppressing an immune response is useful for with neovascularisation of an autoimmune neutropenia, mysathemic lupus experience of an autoimmune thyroiditis, idiopathic Addison's disease, vithigo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, cidiopathic thromboxytopenia purpura, Grave's disease, codeasture's and disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune codense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, hypoproliferative disease. The method is useful in preventing or treating specific proliferative and oncogenic disease, growth deficiency, hypoproliferative disease repulation

Coronic desease conservance, appressis regulation

DB 2; Length 770;

97.9%; Score 1144;

Query Match

hypertension, etc Sequence 770 AA;

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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. ARPF inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
                                                                                                                                                                                                           121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                               250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
                                                                                                                                                           GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
                                                                     1 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSQGDMQDLN
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   Length 769;
                                      4; Indels
   Score 1144; DB 5;
Pred. No. 2.2e-96;
1; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                 AAR82995 standard; protein; 770 AA
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     97.9%;
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Query Match
Best Local Similarity 97.8
Matches 224; Conservative
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N-PSDB; AAT05619.
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                                                                                   130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
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                                                         1 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKWKVVENLODDFDFNYKTLKSQGDMQDLN
                                                                                                                GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                    GNNQSVTRQKWQQLEQMLITALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRRQOI
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                                                                                                                                                                                                                                     VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
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                           Indels
2.2e-96;
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                                                                                                                                                                                                                                                                                                                                          AAY03768 standard; protein; 770
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Matches 224; Conservative
                           Conservative
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            Best Local Similarity
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                                                                                  ACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
GNNQSVTRQXMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                            GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRRQQI
                                                                     ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                       STAT, signal transducer and activator of transcription; crystal; drug design; murine.
                                                                                                              229
                                                                                                                       VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL
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/label= 3(10) helix of alpha helix
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/label= Alpha helix 2
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/label= Alpha helix 5
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than S.O Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal
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Search completed: May 25, 2005, 17:36:37 Job time : 123.057 secs us-10-090-185-29.rai

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1 NHPTAAVVTEKQQMLEQHLQ......IKTGVQFATAVALLVKFPEL 229
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-36-796-12

US-08-82-09-12

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US-08-95-65-12

US-08-96-85-12

US-09-364-970-3

US-09-364-970-5

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US-09-430-806A-3
US-08-852-091-6
US-08-852-091-6
US-08-956-652-6
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US-08-956-652-6
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APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Horvath, Cur M
APPLICANT: Barnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-233
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 199-08-31
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-387-418A-29; Sequence 29, Application US/09387418A; Sequence 29, Extent No. 6391572; GENERAL INFORMATION:
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US-09-387-418A-18
US-09-387-418A-18
Sequence 18, Application US/09387418A
Patent No. 6391572
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: WIZESZYJBKA, Melissa H
  ORGANISM: Mus musculus
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IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 252;
                                        181 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1155; DB 3;
Pred. No. 8.6e-98;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09387418A;
Sequence 9, Application US/09387418A;
Patent No. 6391572;
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING;
CURRENT APPLICATION NUMBER: US/09/387,418A;
CURRENT FILING DATE: 1999-08-31
NUMBER: OF SEQ ID NOS: 43
SEQ ID NO 9
LENGTH: 271
                                                                                                                                                                    US-09-387-418A-14

Sequence 14, Application US/09387418A

Sequence 14, Application US/09387418A

Sequence 14, Application US/09387418A

Sequence 14, Application US/09387418A

Septicant Information:
Applicant Zhang, Xiaokui
Applicant Darnell Jr., James E

TITLE OF INVENTION: INTERFECTIONS

TITLE OF INVENTION: INTERFECTIONS

TITLE OF INVENTION: INTERFECTIONS

TITLE OF INVENTION: INTERFECTIONS

CURRENT APPLICATION NUMBER: US/09/387,418A

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 98.7%;
Matches 226; Conservative
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ORGANISM: Mus musculus
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Best Local Similarity
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LENGTH: 252
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GENERAL INCORNATION:
GENERAL INCORNATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Arcsezczynska, Melissa H
APPLICANT: Horvach, Curt M
APPLICANT: Horvach, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
SUPPRESS OF FEED IN NOS: 43
SUPPRESS OF FEED IN VOS: 43
SUPPRESS OF FEED IN VOE: 2.0
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Pred. No. 7.6e-98;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                              Length 229;
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ilarity 98.7%;
Conservative C
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Best Local Similarity 98.7<sup>3</sup>
Matches 226; Conservative
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US-09-387-418A-28
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Best Local Similarity
Matches 226; Conserv
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US-09-387-418A-18
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LENGTH: 229
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Sequence 12, Application US/08852091
Patent No. 5883228
GENERAL INFORMATION:
APPLICANT: James B. Darnell, Jr.
APPLICANT: Zlong Wen
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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                                                                     190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
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                                              121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                                                             310 VELFRNLMKSAFVVERQPCMPWHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                 181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
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Pred. No. 3.6e-97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Ve. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION ATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 Hackensack Avenue
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REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 98.7
Matches 226; Conservative
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MEDIUM TYPE: Floppy
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STATE: New Jersey
COUNTRY: USA
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US-08-852-091-12
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Patent No. 5716622
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: 21long Wen
APPLICANT: 21long Wen
APPLICANT: 2hong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) FROTEINS
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                                                                                                                                 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                             143
                                                                                                                                                                                                                       ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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                                                                                                                                                                                                                                                                144 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDEELADWKRRPEI 120
                                                                                          83
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                                              1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMODLN
                                                                     24 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMODLN
                                                                                                                                                        84 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
  Gaps
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                                                                                                                                                                                                                                                                                                                                                        VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.8%; Score 1155; DB 1; Length 770; 98.7%; Pred. No. 3.6e-97;
  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSTPTCARTYN
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 438
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUBER: 26,742
REFERENCE/DOCKET NUMBER: 660-1
TELECHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
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TELEX: 133521
INFORMATION FOR SEQ 1D NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 770 amino acids
amino acid
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Matches 226; Conservative
Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
: USA
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Matches
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61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                        310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Boindler, Christian W.
APPLICANT: Boindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
ITILE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1155; DB 2;
Pred. No. 3.6e-97;
0; Mismatches 3;
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US 08/212,185
FILING DATE: 11-WAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
PRIOR APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: WO MESSIVE APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-5EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent No. 5976835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
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Best Local Similarity 98.7%;
Matches 226; Conservative C
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
190 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                              181 VELFRNIMKSAPVVEROPCMPMHPDRPLVIKTGVOFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                   310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                                                                                                  US-08-956-652-12

| Sequence 12, Application US/0895652
| Sequence No. 6013475
| Patent No. 6013475
| GENERAL INFORMATION:
| APPLICANT: Schindler, Christian W. APPLICANT: Fu, Xian-Yuan
| APPLICANT: Fu, Xian-Yuan
| APPLICANT: Fu, Xian-Yuan
| APPLICANT: Rough Zhong
| TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
| TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OFFRAINGS YSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
FILING DATE:
PILING DATE:
PRICK APPLICATION DATA:
PRICK APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 11-MAR-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: US 08/126,588
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vp: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 411 Hackensack Avenue
CITY: Hackensack
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TELEPHONE: 201 487-5800
TELEFAX: 201343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 770 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackenback
STATE: New Jersey
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Length 770;

DB 3;

98.8%; Score 1155;

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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                      190 GNNQSVTRQKOQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                    1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                              61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
                                                                                                   Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
                                                                                                   98.8%; Score 1155; DB 3; 98.7%; Pred. No. 3.6e-97; iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600-1-073 CIP
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
TITLICATION NUMBER: US 07/854,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION UNBER: US 08/126,588
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/08948547
Patent No. 6124118
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CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION:
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                                                                                              Query Match
Best Local Similarity 98.7<sup>1</sup>
Matches 226; Conservative
    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey
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US-08-948-547-12
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                                                                                                   61 GNNOSVTROKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                              250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                               9
                                                                          1 NHPTAAVVTEKOOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLLN
                                                                                                                                                                                                 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                  121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
APPLICANT: Chong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels
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APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAMME: JACKSON ERG., DAVIG A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTR:

ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"AUTITER: IBM PC compatible
"TYPE: "TYPE: PC POS/MS-DOS
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APPLICATION NUMBER: US/08/956,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Klauber & Jackson STREET: A11 Hackensack Avenue CITY: Hackensack STATE: New Jersey COUTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08956869
Patent No. 6030808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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US-08-956-869-12
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COUNTRY: U
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STREET: 41
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Patent No. 6235873

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING FILE REFERENCE: 600-1-25

CURRENT APPLICATION NUMBER: US/09/364,970

CURRENT FILING DATE: 1999-07-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PATENTI VET: 2.0
                                                                                                                                                                                                                                              1 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMQDLN
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                                                                                                                                                                                      Length 770;
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                                                                                                                                                                                   Score 1155; DB 3;
Pred. No. 3.6e-97;
0; Mismatches 3;
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Pred. No. 3.6e-97;
0; Mismatches 3;
12:
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                                                                                                                                                                                    98.8%;
                                                                                        LENGTH: 770 amino acids
TYPE: amino acid
                                                                                                                                                                                 Query Match
Best Local Similarity 98.7
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 226; Conservative
                                                                                                                              / MOLECULE TYPE: protein US-08-948-547-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
                                                                                                                           linear
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Best Local Similarity
                                                                                                                        TOPOLOGY:
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                                                                                   GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 199-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Fu, Xian-Yuan
APPLICANT: Abong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1155; DB 3;
Pred. No. 3.6e-97;
0; Mismatches 3;
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US-09-364-970-5; Sequence 5, Application US/09364970; Patent No. 6235873
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411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 98.8%;
Best Local Similarity 98.7%;
Matches 226; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-5
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: USA
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Patent No. 6605442
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Pu, Xian-Yuan
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                   NAME: Jackson Egg., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-195
RELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                     PRPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SRE-1993
ATTORNEY, AGENT INFORMATION:
APPLICATION NUMBER: . US 07/980,498
FILING DATE: 23-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 770 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 98.73
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                      FILING DATE: 23-NOV-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-956-653A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600-1-073 CIP
                     FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: 26,742
RILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: 3-Ackson BSq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFARX: 201 343-1684
INFORMATION FOR SEQ ID NO: 12:
SEQUIBMOR CHARACTERISTICS:
US/08/212,185
11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 770 amino acids
amino acid
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Search completed: May 25, 2005, 17:47:39 Job time : 28.6534 secs

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May 25, 2005, 17:36:58; Search time 100.287 Seconds (without alignments) 763.830 Million cell updates/sec
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1 NHPTAAVVTEKQQMLEQHLQ.....IKTGVQFATAVALLVKFPEL 229
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1434725 seqs, 334507595 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 29, Appl	Sequence 18, Appl	Sequence 28, Appl	Sequence 14, Appl	9, 4	12	12,	Sequence 31, Appl	Sequence 30, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 8, Appli
QΙ	US-10-090-185-29	US-10-090-185-18	US-10-090-185-28	US-10-090-185-14	US-10-090-185-9	US-09-876-773-12	US-10-639-617-12	US-10-090-185-31	US-10-090-185-30	US-10-380-020-4	US-10-380-020-2	US-10-380-020-5	US-10-045-792-8
DB	13	13	13	13	13	11	17	13	13	15	15	15	14
% Query Match Length DB	229	229	229	252	271	770	770	229	229	720	769	769	770
% Query Match	100.0	98.8	98.8	98.8	98.8	98.8	98.8	98.5	98.4	97.9	97.9	97.9	97.9
Score	1169	1155	1155	1155	1155	1155	1155	1151	1150	1144	1144	1144	1144
Result No.	п	7	m	4	S	9	7	æ	00	10	11	12	13

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Sequence 56, Appl Sequence 2, Appli Sequence 780, App Sequence 780, App Sequence 329, App Sequence 349, App	222, PA	112 A	Sequence 4, Appli Sequence 1, Appli Sequence 14, Appli Sequence 352, App Sequence 19, Appl Sequence 19, Appl Sequence 250, App Sequence 550, Appl Sequence 6, Appli Sequence 6, Appli Sequence 8, Appli
14 US-10-038-010-56 14 US-10-117-087-2 9 US-09-925-302-780 10 US-09-925-302-780 15 US-10-116-275-329 15 US-10-116-275-349			11 US-09-876-773-4 14 US-10-245-120-1 14 US-10-308-279-44 16 US-10-755-889-852 16 US-10-755-889-823 17 US-10-492-043-19 17 US-10-639-617-4 9 US-09-925-295-550 9 US-09-935-246-69 11 US-09-876-773-8
770 770 793 770	213 236 223 185 176 128	749 268 582 712 712 712 712 750	750 750 750 750 750 749
1144 97.9 1144 97.9 1144 97.9 1144 97.9 1141 97.6 1139 97.4	933 70 70 51 51		5556 47.6 5556 47.6 5556 47.6 5556 47.6 5556 47.6 5559 47.6
41 11 11 11 19	20 22 23 24 25 26	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩

## ALIGNMENTS

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Sequence 29, Application US/10090185
; Sequence 29, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
    APPLICANT: Arabay, Xiaokui
    APPLICANT: Arabay, Xiaokui
    APPLICANT: Arabay, Xiaokui
    APPLICANT: Darnell Jr., James E
    TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
    TITLE OF INVENTION: INTERACTIONS
    TITLE OF INVENTION: INTERACTIONS
    TITLE OF INVENTION: UNMBER: US/10/090,185
    CURRENT APPLICATION NUMBER: US/387,418
    PRIOR FILING DATE: 1999-08-31
    NUMBER OF SEQ ID NOS: 43
    SOFTWARE: Patentin Ver: 2.0
    SEQ ID NO 29
    LENGTH: 229
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Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 229; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus musculus
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US-10-090-185-14

i Sequence 14, Application US/10090185

sequence 14, Application US/10090185

sequence 14, Application US/20020197647A1

sequence 14, Application US/20020197647A1

sequence 14, Application Wisson Interpretation No. US20202979684, Melissa H

APPLICANT: Wrzeszczynska, Melissa H

APPLICANT: Horvath, Curt M

APPLICANT: Darnell Jr., James E

ITTLE OF INVENTION: INTERACTIONS

ITTLE OF INVENTION: INTERACTIONS

FILE REPERENCE: 600-1-253

CURRENT APPLICATION NUMBER: US/10/090,185

CURRENT APPLICATION NUMBER: 09/387,418

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SEQ ID NOS: 43

SEQ ID NO 14

SEQ ID NO 14
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                                                                                                            Length 229;
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                                                                                                          Score 1155; DB 13;
Pred. No. 3.2e-93;
0; Mismatches 3;
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                                                                                                            Query Match
Best Local Similarity 98.7%;
Matches 226; Conservative
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Matches 226; Conservative
                     TYPE: PRT
CORGANISM: Mus musculus
US-10-090-185-28
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LENGTH: 229
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wreeszczynska, Melissa H
APPLICANT: Wreeszczynska, Curk
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-253
CURRENT FILING DATE: 2002-03-04
FRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                              APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Curk
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 229
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                                                                                         181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1155; DB 13;
Pred. No. 3.2e-93;
0; Mismatches 3;
                                                                                                                                                                                                                              S-10-090-185-18
Sequence 18, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
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Publication No. US20020197647A1
GENERAL INFORMATION:
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Best Local Similarity 98.7
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Mus musculus
US-10-090-185-18
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.8%; Score 1155; DB 11; Length 770; 98.7%; Pred. No. 1.5e-92; ive 0; Mismatches 3; Indels 0
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Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION PACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                              FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US33/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO 0831/26,588
FILING DATE: 14-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEFAK: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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Publication No. US200050079543A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Klauber
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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Matches 226; Conservative
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US-10-639-617-12
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Sequence 9, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wizeszczyneka, Melissa H
APPLICANT: Wizeszczyneka, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: RECEPTOR RECCCNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1155; DB 13
Pred. No. 3.9e-93;
0; Mismatches 3
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E. Schindler, Christian W. Fu, Xian-Yuan Wen, Zilong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.8%;
Best Local Similarity 98.7%;
Matches 226; Conservative (
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus US-10-090-185-9
                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 9
LENGTH: 271
TYPE: PRT
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US-09-876-773-12
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IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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                                                                                                                                                                                              1 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSQGDMQDLN
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                                                                                                Length 229;
                                                                                                                                               Indels
                                                                                                Score 1151; DB 13;
Pred. No. 7.1e-93;
                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WIZESZCZYJEKA, Melissa H
APPLICANT: HOTVALh, CURT M
APPLICANT: HOTVALh, CURT M
APPLICANT: HOTVALh, CURT M
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
FILE REFERENCE: 600-1-253
FURRENT APPLICATION NUMBER: US/10/090,185
CURRENT APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 2002-03-04
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-185-30
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
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                                                                                              Query Match 98.5%;
Best Local Similarity 98.3%;
Matches 225; Conservative
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Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhang, Xiaokui APPLICANT: Wrzeszczynska
                           ; ORGANISM: Mus musculus
US-10-090-185-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
                                                                                           Query Match
Best Local Similarity
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US-10-380-020-4
; Sequence 4, Ap
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  TYPE: PRT
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Publication No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui

APPLICANT: Horvarh, Outr M

APPLICANT: Horvarh, Outr M

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

CURRENT APPLICATION NUMBER: US/10/090,185

CURRENT APPLICATION NUMBER: 09/387,418

PRIOR PILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFUTARE: Patentin Ver: 2.0

SEQ ID NO 31

LENGTH: 229
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
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98.8%; Score 1155; DB 17
Best Local Similarity 98.7%; Pred. No. 1.5e-92;
Matches 226; Conservative 0; Mismatches 3
                                                                                                       APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-MOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                      APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                           PRIOR APPLICATION DATA
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TOPOLOGY: linear
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APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Joste, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
        GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQ1 249
                                                                                                                  250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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Darnell, Jr., James E.
Kuriyan, John
TITLE OF INVENTION: A CAYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/10380020; Publication No. US20040052762A1; GENERAL INFORMATION:
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Publication No. US20030003563A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
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                                              APPLICANT: Yu, Hua
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Joalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
FURRENT APPLICATION NUMBER: 9210/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
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APPLICANT: PardOll, Drew
APPLICANT: Dave, Richard
APPLICANT: Jove, Millian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10380020 Publication No. US20040052762A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 720
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SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 769
Publication No. US20040052762A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 97.8
Matches 224; Conservative
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US-10-380-020-4
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US-10-380-020-2
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FEATURE:
NAME/KEY: STAT3 : Transcription factor
LOCATION: (1)..(770)
                                         ; LOCATION: (1)..(77;
; OTHER INFORMATION:
US-10-038-010-56
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Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFRENCE: B476.7A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ 1D NOS: 67
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                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-0Ct-2001
CLASSIFICATION NUMBER: US/10/045,792
FILING DATE: 19-0Ct-2001
APPLICATION NUMBER: US/09/012,710
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: JACKEON ESQ., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
TELEFEX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
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             ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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ORGANISM: Homo sapiens

SEQ ID NO 56 LENGTH: 770

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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                            121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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                                                                                                                                  1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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         Length 770;
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                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10117087; Publication No. US20030166854A1; Bublication No. US2003016685A1; Publication No. US2003016685A1; APPLICANT: SERLUPI-CRESCENZI, Ottaviano; APPLICANT: BELLA PIETRA, Linda; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3; FILE REPERENCE: SERLUPI=2 CURRENT APPLICATION NUMBER: US/10/117,087; CURRENT FILING DATE: 2002-04-08; PRIOR APPLICATION NUMBER: US/09/526,542; PRIOR FILING DATE: 2000-03-19; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0; SEQ ID NO 2: LENGTH: 770
      Score 1144; DB 14;
Pred. No. 1.4e-91;
1; Mismatches 4;
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   Query Match 97.9%;
Best Local Similarity 97.8%;
Matches 224; Conservative
Query Match
Best Local Similarity
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US-10-117-087-2
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, usiņg sw model

May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds (without alignments) 1019.898 Million cell updates/sec Run on:

US-10-090-185-29 1169 1 NHPTAAVVTEKQQMLEQHLQ.....IKTGVQFATAVALLVKFPEL 229 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 08 Minimum I Maximum I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

;		de (			SUMMARIES	-
Result No.	Score	Query	Query Match Length	DB	. QI	Description
-	1144	97.9	770	7	4	ISGF3 p91-related
~	1139	97.4	770	~	A54444	DNA-binding protei
m	510.5	43.7	739	~	A46159	interferon-depende
4	495	42.3	748	N	A56047	gamma-interferon a
ഗ	310	26.5	851	~	A46160	interferon alpha-i
9	269.5	23.1	786	~	I49274	mammary gland fact
7	269.5	23.1	793	7	S54772	
80	263.5	22.5	794	~	G02317	transcription acti
σ	238	20.4	794	~	S55527	mammary gland fact
10	126	10.8	978	~	A70387	conserved hypothet
11	124	10.6	533	~	G72593	hypothetical prote
12	122	10.4	848	~	A54740	interleukin-4-indu
13	120.5	10.3	837	~	157557	DNA-Binding Protei
14	119.5	10.2	1166	~	T27075	hypothetical prote
15	118.5	10.1	1208	~	AE1947	chromosome segrega
16	118.5	10.1	2094	~	833124	tpr protein - huma
11	115.5	6.6	924	7	S06117	
18	115	8	1164	~	T24806	
19	114.5	8.6	2007	Н	B43402	
50	114	9.8	7	7	A59252	
21	113.5	9.7		~	AC1814	hypothetical prote
22	113.5	9.7		~	S33821	n body p
23	112.5	9.6	946	7	S28061	SCP1 protein - rat
24	112.5	9.6	1690	~	T13030	microtubule bindin
52	112.5	9.6	1957	7	T38077	hypothetical coile
56	112.5	9.6	2253	~	T30336	nuclear/mitotic ap
27	112	9.6	289	~	851193	
28	112	9.6	1509	H	A27224	heavy
53	112	9.6	1999	гH	S21801	myosin heavy chain

RESULT 2 A54444 DNA-binding protein APRF - human

M protein - Helico exonuclease (EC 3.	myosin heavy chain	kinesin-related pr	myosin heavy chain	myosin heavy chain	chromosome segrega	hypothetical prote	hypothetical prote	myosin heavy chain	hypothetical prote	epidermal growth f	ATP-dependent dsDN	ATP-dependent dsDN	interaptin - slime	dystrophin, muscle
C64527 BVECSC	A33977	A57107	A59287	A47297	G83960	T21174	T43448	833068	T27055	S43074	C85535	G90684	T14867	A27605
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284 1048	1959	747	1940	1992	1188	2020	434	527	734	968	1047	1047	1738	3685
0 0 0 0.	9.5	9.5	9.5	9.5	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4
111.5	111	110.5	110.5	110.5	110	110	109.5	109.5	109.5	109.5	109.5	109.5	109.5	109.5

## ALIGNMENTS

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Library pyl-Tetaled transcription ractor - mouse Library pyl-Tetaled transcription ractor - mouse Library pyl-Tetaled transcription ractor - mouse Cipate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 Cipate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 Cipate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 Cipates 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 Cipates 02-Jul-1996 #sittle: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p9l-related tr A;Reference number: A54444; MUID:94208062; PMID:7512451 A;Reference number: A54444; MUID:94208062; PMID:7512451 A;Reference number: Levy, D.E. A;Cross-references: UNIPROT:P42227; GB:L29278; NID:9476715; PIDN:AAA37254.1; PID:947671 R;Rez, R.; Durbin, J.E.; Levy, D.E. J. Biol. Chem. 269, 24391-24395, 1994 A;Title: Acute phase response factor and additional members of the interferon-stimulate: A;Reference number: 149009; MUID:95014185; PMID:7523373 A;Accession: 149009 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-393, M', 395-700, 702-770 <REZ. A;Cross-references: EMBL:U08378; NID:9473889; PIDN:AAA56668.1; PID:9473890 C;Genetics: Apper RMBA A;Residues: 1-393, M', 395-700, 702-770 <REZ. A;Cross-references: EMBL:U08378; NID:9473889; PIDN:AAA56668.1; PID:9473890
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ISGF3 p91-related transcription factor - mouse
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A;Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; PID:g1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in
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C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: A54444
C;Accession: A54444
C;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud (Call 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transfacence number: A54444; MUID:94208062; PMID:7512451
A;Accession: A54444
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: A54444
A;Residues: 1-770 <RES>
A;Cession: A54444
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:9475789; PID:9475789
C;Genetics:
C;Genetics: CBB:358950
A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:358950
A;Map position: 17921-17921
C;Suporfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rischindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A; Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG
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Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004; Accession: A46159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 770;
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A;Accession: A46159
A;Status: preliminary; not compared with conceptual tran
A;Molecule type: nucleic acid; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.7%; Score 510.5; DB 2; ilarity 44.9%; Pred. No. 1.4e-26; Conservative 49; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1139; DB 2;
Pred. No. 2.3e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 97.4%;
Matches 223; Conservative
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Best Local Similarity
Matches 101; Conserva
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C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56047
R;Accession: A56047
Mol. Cell. Biol. 14, 4342-4349, 1994
Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e. A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Rether preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-748 <XAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P42228; GB:U09351; NID:9509502; PIDN:AAA19692.1; PID:950950
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QVRQQLKKLEELEQKYTYEHDPITKNKQVLWDRTFSLF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 VTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKS--QGDMQDLNGNNQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 748;
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                                                                                                                                                                                                                                     gamma-interferon activation site-binding protein Stat4 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
                                                                                   299 QQLIQSSFVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQEL
                                                      185 RNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.3%; Score 495; DB 2; 44.2%; Pred. No. 1.6e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99; Conservative
  250 GPPNACLDQLQ----
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A;Residues: 1-851 <YAN>
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63

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mammary gland factor - mouse

NyAlternate names: stat5 protein
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S54772; 149273
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
BMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Accession: S54772
A;Status: preliminary, nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-793 <MUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:248538; NID:g758633; PIDN:CAA8 R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L. Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
                                                               137 MSQKHLQINQRPBELRLITQDTENELKKLQQTQEYFIIQYQESLRIQAQFAQLGGLNPQE 196
                                                                                                                                                        -----QSVTRQKMQQLEQML----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELA 112
                                                                                                                                                                                                              194 POERMSRETALOOKOVSLETWLOREAQTLOOYRVELAEKHOKTLOLLRKQOTIILDDELI 253
                                                                                                                                                                                                                                                                          113 DWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 QWKRRQQLAGNGGPPEGSLDVLQSWCEKLABIIWQNRQQIRRAEHLCQQLPIPG-PVEEM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 RMSRETALOOKOVSLETWLOREAQTLOOYRVELAEKHOKTLOLLRKOOTIILDDELIOWK 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription activator stat5A - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
                                      AAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNY-KTLKSQGDMQDLNGNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: U21103; NID: 9747971; PIDN: AAA80590.1; PID: 9747972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: human signal transducer and transcription activator STATSA
                                                                                                                                                                                                                                                                                                                                                                                                                                        313 LAEVNATITDIISALVTSTFIIEKQP------PQVLKTQTKPAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                                                               173 RPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLV 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 VNATÍTDIISALVTSTFIIĒKOP-----POVLKTOTKFAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.1%; Score 269.5; DB 2; Best Local Similarity 30.6%; Pred. No. 1.7e-10; Matches 70; Conservative 42; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Regidues: 1-793 <RES>
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C;Superfamilw:
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A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin A;Reference number: S54772; MUID:95237198; PMID:7720707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.Alternate names: STATS protein homolog p80
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-011-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149274; S54773; S6005 Musculus homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
A;Accession: 149274
A;Accession: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-432, 'E', 434-786 <MUI>
A; Residues: 1-432, 'E', 434-786 <MUI>
A; Ricoss-references: EMB::248339; NID::9758635; PIDN:CAA88420.1; PID::9758636
R; Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,
EMBO J. 14, 1402-1411, 1995
A; Title: Interleukin-3 signals through multiple isoforms of Stat5.
A; Reference number: S54725; MUID:95246733; PMID:7537213
                                               A.Status: nucleic acid sequence not shown
A.Ratus: nucleic acid sequence not shown
A.Racidues: 1-196;332-591;684-730 < YAW>
A.Racidues: 1-196;332-591;684-730 < YAW>
A.Cross-references: EMBL:U18671
C;Genetics:
A.Gene: stat2
A.Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2;
C;Superfamily: human signal transducer and transcription activator STATSA
C;Keywords: signal transduction; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 NICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 VTEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               . 9
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                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 851;
                                                                                                                                                                                                                                                                                                                                                                                                                            92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 MKSAFVVEROPCMPMHPDRPLVIKTGVQFATAVALLVKFPE 228
Reference number: $53873; MUID:95192056; PMID:7885841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S54773
A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 23.1%; Score 269.5; DB 2; Best Local Similarity 30.6%; Pred. No. 1.7e-10; Matches 71; Conservative 42; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                            51; Mismatches
                                                                                                                                                                                                                                                                                                                                                               26.5%; Score 310; 32.6%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues: 1-432,'E',434-786 <AZA>
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 32.69
1es 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-786 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mammary gland factor
                            Accession: S53873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S54727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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5,

Gaps

21;

Length 793;

D.E.; O

9

281

7;

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A;Residues: 1-978 <AQF>
A;Cross-references: UNIPROT:067124; GB:AE000718; NID:g2983504; PIDN:AAC07092.1; PID:g29:A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nypothetical protein APB1216 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Accession: G72293
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jan-no, K.; Taka bNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9YCP2; DDBJ:AP000061; NID:g5104821; PIDN:BAA80205.1; PID:d
A;Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                             Nature 392, 353-358, 1998

Affile: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A/Atile: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A/Accession: A70387

A/Accession: A70387

A/Status: prellminary; nucleic acid sequence not shown; translation not shown A/Molecule type: DNA

A/Residues: 1-978 <AQF>
                                                                                                                                                                                                                         conserved hypothetical protein aq_1006 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A70387
R;Deckert, G:; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 KMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLT--------------------DEELAD- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 RIBEIDKKLTELKVRKNKLTKELAVLKDELSFAQEELNRIEAEKEKFKEEKEREKELEHR 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 WKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DFNYK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 EKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                             316 VNATITDIISALVTSTFIIEKQP------PQVLKTQTKFAATVRLLV 356
                                176 LEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 10.8%; Score 126; DB 2; Length 978; Local Similarity 23.8%; Pred. No. 0.77; les 50; Conservative 38; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.6%; Score 124; DB 2; Length 533; Best Local Similarity 21.2%; Pred. No. 0.52; Matches 42; Conservative 49; Mismatches 65; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:: ||: | :: || :::|| | 234 EEKDSLERELSQVVTKLKELENLEKEVEKLREKLEREKLEFSRKVAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 VTEKQQMLEQHLQDVRKRVQDLEQKMKVVEN----LQDDF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 BEKLEKIKELFSBERYTSLKMKERLLVELQ 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 PMLEERIVELFRN-----LMKSAFVVERQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-533 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: DNA
A, Residues: 1-533 < K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: aq 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                               mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55527; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
R;Wakao, H.; Gouilleux, F.; Groner, B.
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula
A;Reference number: S55527; MUID:95188889; PMID:7882987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-794 «WAK.
A; Cross-references: UNIPROT: P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g6023
A; Note: this is a revision to the sequence from reference S44353
R; Wakao, H.; Gouilleux, F.; Groner, B.
BMBO J. 13, 2182-2191, 1994
A; Title: Manmary gland factor (MGF) is a novel member of the cytokine regulated transcri
A; Reference number: S44353; MUID:94244619; PMID:7514531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 NGNNQSVTRQKMQQLEQML----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 RLSRETALQÓKQVSLEAWLQREAQTLQÓYRVELAEKHOKTLÓLLRKQÓTIILDDELIQWK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                          8 VIEKOOMLEOHLODVRKRVQDLEOKWKVVENLODDFDFNY-KTLKSQGDMQDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 VTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNY-KTLKSOGDMODLNGNN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----QSVTRQKMQQLEQML----TALDQMRRSIVSELAGLL,SAMEYVQKTLTDEELADWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: this sequence has been revised in reference S55527 Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 VNATITDIISALVTSTFIIEKQP-----PQVLKTQTKFAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 LEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLV 224
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llarity 29.3%; Pred. No. 2.1e-08;
Conservative 42; Mismatches 98; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-716,'RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>;Cross-references: EMBL:X78428
                                                       submitted to the EMBL Data Library, December 1995
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Best Local Similarity
Matches 67; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: mRNA
Accession: G02317
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6/3; 240/2; 288/2; 594/2; 657/3; 756/3; 798/2; 900/3; 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome segregation protein [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------KKLQRLREDLVLEKSRRADLIGRIHSLCTTLSLN 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- WKRRPEIACIGGPPNI ----- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDIMMNALVAVKRERDDLRIQGNQQIQELHDLKRDIEKLRRSE 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLQTRQQI----KKLEELQQKVSYKGDPIVQHRPMLEERIVEL 183
                                                                                                           KMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELA 112
                                                                                                                                                                                        CLDRLENWITSLAESQLQTRQQIKKLE-ELQQKVSYKGDPIVQ 171
                                                                                                                                                                                                                                                                    NGNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEY- 101
                                                                                RVQD------LEQKMKVVENLQDDFDFNYKTLKSQGDMQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nn
evision 15-Oct-1999 #text_change 15-Oct-1999
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                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                 KSAFVVEROPCMPMHPDRPLVIKTGVQFATAVALLV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73;
                                         83; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 119.5; DB 2; Length 1166;
; Pred. No. 2.6;
46; Mismatches 72; Indels 73;
Score 120.5; DB 2; Length 837; Pred, No. 1.5; 31; Mismatches 83; Indels 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                - Caenorhabditis elegans
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                       A;Residues: 1-1208 «KUR»
A;Cross-references: UNIPROT:Q8YXT3; GB:BA000019; PIDN:BAB73085.1; PID:g17130474; GSPDB:G
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 23.9%; Pred. No. 3.1;
Matches 55; Conservative 44; Mismatches 82; Indels 49;
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A;Gene: alr1128
C;Superfamily: chromosome segregation protein SMC1
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C; Accession: AE1947
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089w24 P42228 Q7zz53 Q8w20 Q7zz77 Q8jfu7 Q66hb2 Q8jf85

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Perfect score:

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Sequence:

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Result Š.

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TISSUBERCE FROM N.A. (ISOPORMS 1 AND DEL-701).

TISSUBERCATURE: 2128825; PubMed=1247932; DOI=10.1073/pnas.242603899;

MEDLINE: 2128825; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MREDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
Yoshida K., Sudo T., Naruto M., Kishimoto T.;
"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gp130-mediated signaling
cell 77:63-71(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
Rajkumar N., Yi Q., Nickerson D.A.;
"SeattleSNPs. NHLBI H46682 program for genomic applications, UW-
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
"Highly conserved amino-acid sequence between murine STAT3 and a
revised human STAT3 sequence.";
Gene 213:119-124(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                           STA3_HUMAN STANDARD, PRT; 770 AA.
P40763; 014916; Q9BW54;
01-FBB-1995 (Rel. 31, Created)
05-UTL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                   ALIGNMENTS
08JFU8
0801Y2
0801Y2
STA4 HUMAN
090Y1
031312
08AW24
07ZZ53
07ZZ57
08AW20
07ZZ77
08JFU7
08JFU5
09G6HB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
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Homo sapiens (Human).
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                                NCBI_TaxID=9606;
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1 NHPTAAVVTEKQQMLEQHLQ......IKTGVQFATAVALLVKFPEL 229
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                1612378 seqs, 512079187 residues
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GO:0005634; C:nucleus; TAS.
GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                         Giraud S., Bienvenn F., Avril S., Gascan H., Heery D.M., Coqueret O., "Functional interaction of STAT3 transcription factor with the coactivator NGOA/SRC1a.",
J. Biol. Chem. 277:8004-8011(2002)
J. Biol. Chem. 277:8004-8011(2002)
J. FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "ISOUGHE 940763-2; Sequence=VSP_010474;
-1-TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.
-1- FTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.
-1- SIMILARITY: Belongs to the transcription factor STAT family.
-1- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                               MEDLINE-95215843; PubMed-7701321; Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S., I. Requirement of serine phosphorylation for formation of STAT-promoter complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: Involved in the gpl30-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI.
-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                        Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                              PubMed=11773079; DOI=10.1074/jbc.M111486200;
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EMBL, AY572796, AAS6696.1;
EMBL, BC000627, AAH00627.1;
EMBL, BC014482, AAH14402.1;
EMBL, AF029311; AAB84254.1;
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                                                                                                                                           SEQUENCE OF 564-704 FROM N.A.
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Genew; HGNC:11364; STAT3.
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphotyrosine (by JAK) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH2 domain; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c; TISSUE-Liver;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
R GO; GO:0003700; F:transcription factor activity; TAS.

GO; GO:0006928; P:cell motility; TAS.

GO; GO:0007259; P:cell motility; TAS.

R GO; GO:0000122; P:negative regulation of transcription from P. ..

R GO; GO:0007165; P:negative regulation of transcription from P. ..

R GO; GO:0007165; P:negative regulation of transcription from P. ..

R GO; GO:0007165; P:negative regulation of transcription from P. ..

R GO; GO:0007165; P:selgnal transduction; TAS.

R InterPro; IPR0009867; PS3_like_DNA_bnd.

R InterPro; IPR00127; STAT.

R Pfam; PF00017; STAT_lin.

R Pfam; PF00017; STAT_lin.

R Pfam; PF000665; STAT_lin.

R Pfam; PF000665; STAT_lin.

R PROSITE; PS50001; SH2: 1.

W Activator; Alternative splicing; DNA-binding; Nuclear protein; Proceeding Processing Command Comma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-21004 (Rel. 45, Last amnotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.9%; Score 1144; DB 1; Length 770; 97.8%; Pred. No. 4.3e-62; ive 1; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphoserine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform Del-701)/
/FIId=VSP_010474.
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/FTId=VAR 018683.
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V -> L (in Ref. 1).
T -> A (in Ref. 1).
Y; 6C00632211C8012D C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O -> H (in Ref. 1)
P -> S (in Ref. 1)
K -> N (in Ref. 1)
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/FTId=VAR
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Name=Stat3; Synonyms=Aprf;
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nes 224; Conservative
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770 AA;
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ID STA3 MOUSE
AC P42227;
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STRAIN=FVB/N; TISSUE=Mammary gland;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=1287932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=1287932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=1287932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=1287939;

MEDLINE=22388257; PubMed=1287939;

MEDLINE=22388257; PubMed=1287939;

MEDLINE=22388257; PubMed=1287939;

MEDLINE=22388257; PubMed=1287939;

MEDLINE=22388257; PubMed=1287939;

MEDLINE=2288257; PubMed=1287979;

MEDLINE=2288257;

MEDLINE=2288257;

MEDLINE=2288257;

MEDLINE=2288257;

                                                                                                                                                                                                                                                                                                                   MEDLINE=95014185; PubMed=7523373;
Raz R., Durbin J.E., Levy D.E.;
"Acute phase response factor and additional members of the interferon-stimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T.; "Molecular cloning of ARRF, a novel IRW-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling
                                                                                                                                                                                   Zhong Z., Wen Z., Darnell J.E. Jr., "Stat1: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6."; Science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and CS7BL/6; TISSUB=Liver;
MEDLINE=9601116; PubMed=7568080;
SChaefer T.S., Sanders L.K., Nathans D.;
"Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J, and NOD/LtJ;
Davoodi-Semiromi A., She J.-X.;
A mutant Stat5b with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
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                                                                                                                                SEQUENCE FROM N.A. (ISOFORM STAT3A).
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                                                                                                                                                                     MEDLINE=94188718; PubMed=8140422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zebrafish to mouse.";
                                                                                           Cell 77:63-71(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129/SvJ;
                                                                                                                                                 TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     form of Stat3.
                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
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REPLIMES 99334-005 pubMed-4734024; DOI-10.1016/0092-8674(95)90311-9; Wen Z., Zhong Z., Darnell J.E. Tr. Waxinal activation of transcription by Statl and Statl requires both trytoals and ecrise phosphorylation."; Education of transcription by Statl and Statl requires both trytoals and ecrise phosphorylation."; Education of transcription."; Education of transcription."; Education of transcription."; Education of transcription."; Education."; Education."; Education."; Education."; Education."; Education."; Education."; Education. Educat
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                                                                                                                Phosphotyrosine (by JAK) (By similarity).
                                                                                                                               Phosphoserine.
TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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                                                                                                                                                                                                          Missing (In isoform Del-701).
/Frida-808P 010475.
S-A: Decreased transcriptional activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.9%; Score 1144; DB 1; Length 770; 97.8%; Pred. No. 4.3e-62; ive 1; Mismatches 4; Indels (
Pfam, PF02865; STAT int; 1.
PROSITE, PS50001; SH2; 1.
3D-structure, Activator; Acute phase; Alternative splicing; Direct protein sequencing; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain; Transcription regulation.

FARST CAMPAGE CONTRACTOR C
                                                                                                                                                                                                                                                                         -> K (in Ref. 2).
-> T (in Ref. 2 and 4).
-> I (in Ref. 1).
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01-0CT-1996 (Rel. 34, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                           FTId=VSP 006287.
                                                                                                                                                                                 Stat3B)
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Best Local Similarity 97.8
Matches 224; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACIGGPPNICLDRLENWITSLARSQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                  "Transcription factors Stat3 and Stat5b are present in rat liver nuclei late in an acute phase response and bind interleukin-6 response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACRICAPANTES PROTOCOLD TO ACRICATE AND ACRICAPANTES OF VALIDAR COLOR ACRICAPANTES OF VALIDAR ACRICAPANTES OF VALIDAR ACRICAPANTES OF ACRICAPAN
                                                                                                                                                                                                                                                                                                                     elements.";
J. Biol. Chem. 270:2998-30006(1995).
J. Biol. Chem. 270:2998-30006(1995).
J. FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
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Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SMART; SM0252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              705 705 Phosphotyrosine (by JAK) (By 727 727 Phosphoserine (By similarity) 770 AA; 88039 MW; D74A0C76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGD; 3772; Stat3.
LnterPro; IRR008967; P53 like_DNA_bnd.
InterPro; IPR0008960; SH2_
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X91810; CAA62920.1; -. HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation.
DOMAIN 580 670
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NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                            PROSITE; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFDFYYTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphotyrosine (by JAK) (By similarity)
Phosphoserine (By similarity).
9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.3%; Score 1137; DB 1; Length 770; 97.4%; Pred. No. 1.1e-61; ive 1; Mismatches 5; Indels
                             05-UTL-2004 (Rel. 44, Created)
05-UTL-2004 (Rel. 44, Last sequence update)
05-UTL-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                          TISSUE-Nammary gland;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ620655; CAF06182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activator; DNA-bindamy, Transcription regulation.
DOMAIN 580 670
MOD RES 705 727
MOD_RES 727 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 97.4%;
Matches 223; Conservative
         STANDARD;
                                                                                          Bos taurus (Bovine).
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                              Bovinae; Bos.
NCBI_TaxID=9913;
         BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250
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                       P61635;
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PRT;

PRELIMINARY;

Q6DV79; Q6DV79

06DV79 ID 06 AC 06

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131 HPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLNG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 NNQSVTRQKMQQLEQMLTALDQMRRGIVSELAGLLSAMEYVQKMLADEELADWKRRQQIA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 CIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 HPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNG
                                                                                                                              Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
Asashina M., Yokota T.;
"Activation of Stat3 by cytokine receptor gpl30 ventralizes Xenopus embryos independent of BMP-4";
Dev. Biol. 216.481-490(1999).
EMBL; AB017701; BAA86061.1; -.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Zhou G.Y., Leung F.C.;

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AK641397, AA764887.1; -.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004871; F:signal transducer activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:000742; P:intracellular signaling cascade; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 ELFRNLMKSAFVVERQPCMPMHPDRPLVFKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1119; DB 2; Length 771;
Pred. No. 1.5e-60;
1; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50001; SH2; 1.
771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel 28, Last annotation update)
Signal transducer and activator of transcription 3.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 69/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008967; P53 like DNA_bnd
InterPro; IPR000980; SH2.
InterPro; IPR01217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT int; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.7%;
96.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 96.1
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                             Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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Generation and initial analysis of more than 15,000 full-length human
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                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                            Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stat3 protein.
                   CDNA
                                                                                                                                                 initiative.
                   monse
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Strausberg R.L. Feingold E.A. Grouse L.H., Derge J.G.
Altauner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jeeberg B., Rutchen K.H., Haleh F.,
Distchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Richards A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                               121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                              250 ACIGGPPNICLDRLENWITSLAESQLQIRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
             R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0007242; P:signal transducer activity; IEA.

R GO; GO:0007242; P:intracellular signaling cascade; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000990; SH2.

R InterPro; IPR001217; STAT.

R Pfam; PF00017; STAT.

R Pfam; PF0017; STAT.

R Pfam; PF0017; STAT.

R Pfam; PF0017; STAT.

R Pfam; PF001865; STAT.

R Pfam; PF02864; STAT.

R Pfam; PF02865; STAT.

R Pfam; PR02865; STAT.

R Pfam; PR02865; STAT.

R Pfam; PR02865; STAT.

R PRAM; RNART: SM00252; STAT.

R PROSTIE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                130 SHPNAAVTEKQQMLEQHLQDVRKKVQDLEQKMKVVENLQDDFPFNYKTLKSQSDLSELN
                                                                                                                                                                                                                                                                                                                                                                                   190 GNNQSVTRQKMQQLEQMLTALDQLRRTIISDLASLLSAMEYVQKTLTDEELADWKRRQQI
                                                                                                                                                                                                                                                                                                          1 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
                                                                                                                                                                                                                                                                                                                                                                      GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                     Length 769;
                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                    92.9%; Score 1086; DB 2; 91.7%; Pred. No. 1.5e-58;
                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            766 AA.
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24,
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01-UN-2003 (TYEMBLrel. 2:
01-UN-2003 (TYEMBLrel. 2:
01-MAR-2004 (TYEMBLrel. 2:
Stat3-A protein.
                                                                                                                                                                                                                                                    Query Match 92.9
Best Local Similarity 91.7
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         61
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189
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GO; GO: 0005634; C:nucleus; IEA.

GO; GO: 0004871; F: stagnal transducer activity; IEA.

GO; GO: 0007421; F: stagnal transcription factor activity; IEA.

GO; GO: 0007242; P: intracellular signaling cascade; IEA.

GO; GO: 0007242; P: intracellular signaling cascade; IEA.

GO; GO: 0006355; P: regulation of transcription, DNA-dependent; IEA.

BR InterPro; IPR000980; FH2.

RIME**PRO; IPR001217; STAT.

R Pfam; PF0017; STAT.

R Pfam; PF018017; STAT.

R Pfam; PF02864; STAT.

R Pfam; PF02865; STAT.

R SWART; SM02525; SH2; 1.

R PROSITE; PS550001; SH2; 1.

R PROSITE; PS550001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHPNAAVITEKQQMLEQHLQDVRKKVQDLEQKMKVVENLQDDFDFNYKTLKSQSDLSELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Autaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Autinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                             Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.6%; Score 1083; DB 2; Length 766; 90.8%; Pred. No. 2.3e-58; ive 11; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUB-Embryo;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC044717; AAH44717.1;
HSSP; P42227; 1BG1.
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R., Hong
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                       Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carannor P., Frange C.,

Rables S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKernan K.J., Maranson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garrinci P. Prange C.,

Richards S., Worley K.C., Hale S., Garrina A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rackiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,

Noriski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial amlysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
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GO: GO: GO: GO: GO: F: Endolaus; IEA.
GO: GO: GO: GO: GO: F: F: GO: F: F: GO: F: F: GO: F: F: GO: F: GO:
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Signal transducer and activation of transcription factor 3.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO45-2776; AAH45276.1; --
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.4%; Score 998; DB 2;
83.5%; Pred. No. 1.9e-53;
:ive 21; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              765 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZDB-GENE-980526-68; stat3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 83.5%
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Q6DVF3
   RAPARA RA
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190 GNSQAAATRQKWAQLEQMLSALDQLRRQIVTEMGGLLTAMDYVQKNLTDEELADWKRRQQ 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 HPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                                                                                                                                                                  EMBL, AY639947; AAT64912.1; -. GO; GO:0005634; C:nucleus; IEA. GO; GO:0004871; F:signal transducer activity; IEA. GO; GO:000704871; F:transcription factor activity; IEA. GO; GO:0007242; P:intracellular signaling cascade; IEA. GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Signal transducer and activator of transcription gisoform 1.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Acanthomorpha; Acanthomopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu R., Hong Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX641434; AAT46134.1; -
GO, GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007421; P:iranscription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; PS3_like_DNA_bnd.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.4%; Score 998; DB 2; Length 76.83.5%; Pred. No. 3.8e-53; ive 20; Mismatches 16; Indels
                                                                                                                                                                        Liu R., Hong Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87566 MW; F5D01408748EC703 CRC64;
                                                                                                                                                                                                                                                                                                  GO; GO:0004871; F:signal transducer ac
GO; GO:0003700; F:transcription factor
GO; GO:0007342; P:intracellular signal
GO; GO:0006355; P:regulation of transc
InterPro; IPRO08967; P53 like_DNA_bnd.
InterPro; IPRO01217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PP00017; SH2; 1.
Pfam; PP01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PP02865; STAT int; 1.
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Pfam; PF01017; STAT_alpha; 1.
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                                                                    NCBI_TaxID=8090;
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Name=stat3;
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Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soarse M.B., Bonaldon M.F., Carannori P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Glibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                61 GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
                                                                                                                                                                                                                                    120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                          2 HPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN 60
                                                                                                                                         130 HPTGTVVTEKQQILEHNLQDIRKRVQDMEQKMKMLENLQDDFDFDFNYKTLKSQGELNQDLN
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                2;
                                                                                                                                                                                                                                                                                          180 IVELFRNIMKSAFVVEROPCMPMHPDRPLVIKTGVOFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                                                                    310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTNKVRLLVKFPEL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                    Length 785;
                                                                                              16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC068320; ADR-68320.1; -..
ZFIN; ZDB-687E-980526.68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
                                      785 AA; 89643 MW; 81F231BDE27DE938 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                   85.4%; Score 998; DB 2; 83.5%; Pred. No. 3.9e-53;
                                                                                              20; Mismatches
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last anno
Pfam; PF02864; STAT bind; 1. Pfam; PF02865; STAT int; 1. PROSITE; PS50001; SH2; 1.
                                                                                              Matches 192; Conservative
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NCBI_TaxID=7955;
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                                         SEQUENCE
                                                                   Query Match
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Q6NV46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 HPTGTVVTEKQQILEHNLQDIRKRVQDMEQKMKMLENLQDDFDFNYKTLKSAGELSQDIN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEBLQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPIIQHRPALEEK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thesis (1998), University of Melbourne, Australia.

Thesis (1998), University of Melbourne, Australia.

RASP, P42227, 1861.

RASP, P42227, 1861.

ROSPOSSA, CRUCLEUS, IEA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003700; F:transcription detcor activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:000775; P:intracellular signaling cascade; IEA.

ROSP GO:0000770; PRO00980; SH2.

InterPro; IPR00197; STAT.

Refam; PF001017; STAT alpha; 1.

Refam; PF01017; STAT alpha; 1.

Refam; PF02665; STAT int; 1.

Refam; PF02665; STAT int; 1.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000242; P:intracellular signaling cascade; IEA.
GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000390; SH2.
InterPro; IPR001217; SH2.
InterPro; IPR001217; STAT.
Pfam; PF0017; STAT_alpha; 1.
Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_int; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                              85.4%; Score 998; DB 2; Length 786; 83.5%; Pred. No. 3.9e-53; live 21; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 806;
                                                                                                                                                                                                                                                                                                                                            90039 MW; FC7371D0B0E5447E CRC64;
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92151 MW; 74BC4EA401C3C942 CRC64;
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Last sequence update)
Last annotation update)
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Pred. No. 4e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 83.5
Matches 192; Conservative
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                                                                                                                                                                                                                                                                                                          PROSITE; PS50001; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH2;
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                                                                                                                                                                                                                                                                                                                                            786 AA;
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Best Local Similarity
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Local Similarity
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                                                                                                                                                      NCBI_TaxID=8022;
                                                                                              Name=rbtStat3;
                                                 01-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 185;
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                                               189
                                                                                                                  IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                 GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
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                                                                                HPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                    GNNQ-SVTROKMOQLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
Fam; PF0017; SHZ; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02864; STAT_bind; 1.
SMART; SM00252; SHZ; 1.
PROSITE; PS50001; SHZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87411 MW; E661FFE18BEFD8BE CRC64;
                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.3%; Score 974; DB 2;
82.2%; Pred. No. 1.1e-51;
                                                                                                                                                                                                                                                764 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Mismatches
 Mismatches
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 21;
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Matches 189; Conservative
  Conservative
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NGNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDEBLADWKRRP 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 QIACIGGPPKICLDRLETWITSLGEIOLOIRQQIKKLEELQQKVSYKGDPIIQHRPALEE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                            Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFATAVALLVKPPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 KIVDLFRNLMKSAFVVERQRCMPMHPDRPLVIKTGVQFTNKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Signal transducer and activator of transcription (Fragment)
Name=STAT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Indels
                                                                                                                                                                                                                                                                                           Arredondo J.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IFRULIA.,
PEam; PF01017; SHZ; 1.
PEam; PF01017; STAT_albha; 1.
PEam; PF02864; STAT_bind; 1.
PEam; PF02865; STAT_int; 1.
PEam; PF02865; STAT_int; 1.
                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.1%; Preu. ...
ive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR008967; PS3 like_DNA_bnd.
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
                                          Created)
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.58;
                                                          01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15,
                                          04,
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NCBI_TaxID=9544;
PRELIMINARY;
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EMBL; AF227560; AAF73401.1; -.

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                                                                                                                                                                                                                                                                                                                         162 VSYKGDPIVOHRPMLEERIVELFRNIMKSAFVVEROPCMPMHPDRPLVIKTGVOFATAVA 221
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                                                                                                                                                                                                                                                                                            0; Gaps
                       GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004870; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPRO08967; PS3 like_DNA_bnd.
InterPro; IPRO01217; STAT_
FEAM; PF01017; STAT_alpha; 1.
Pfam; PF01017; STAT_alpha; 1.
NON TER
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SEQÜENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;
                                                                                                                                                                                                                                                    Ouery Match 54.7%; Score 639; DB 2; Length 163; Best Local Similarity 96.1%; Pred. No. 6.9e-32; Matches 123; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: May 25, 2005, 17:43:43 Job time: 96.284 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 LLVKFPEL 229
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                              OM protein - protein search, using sw model
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May 25, 2005, 17:14:45 ; Search time 121.891 Seconds (without alignments) 726.619 Million cell updates/sec 1 NHPTAAVVTEKQQMLEQHAQ......1KTGVQFTTKVRLLVKFPEL 229 2105692 segs, 386760381 residues Gapop 10.0 , Gapext 0.5 US-10-090-185-30 **BLOSUM62** Perfect score: Scoring table: Sequence: Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A\_Geneseq\_16Dec04:\* geneseqp2001s:\* geneseqp2002s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Aay72862 Mouse Sta	Aay72850 Mouse Sta	Aay72846 Mouse Sta	Aay72841 Mouse Sta		Aaw03176 Mouse STA	Aay72863 Mouse Sta	Aae22055 Human Sta	7164 Mouse isc	2054 Human Sta	Aae22056 Human pro	Mouse	Aay03768 Human STA	Aab12377 N-termina	4652 Murine ST	9497 Human bai	Abul0476 Mouse STA	Adn04365 Antipsori	Adp54789 Human PRO	8442 Lung canc	Add44738 Rat Prote		Mouse	2993 Human pla	9964 Human sig
	Deac				-		•		•	4 Abb57164	4 Aae22054		5 Aar82995			2 Aae14652	7 Abg69497		•		2 Aab58442		1 Aay72861			4 Aab19964
	QI .	AAY72862	AAY72850	AAY72846	AAY7284	: AAR72082	AAW03176	AAY72863	AAE22055	ABB57164	AAE22054	AAE22056	AAR82995	AAY03768	AAB12377	AAE14652	ABG69497	ABU10476	ADN04365	ADP54789	AAB58442	ADD44738	AAY72861	AAY72860	AAR82993	AAB19964
	Match Length DB	229 4	229 4	252 4	271 4	770	770 2	229 4	720 5	3 692	5 694	169	770 2	770 2	770 3	770 5	770 5	770 6	770	770	793 3	7 0 7 7	228 4	229 4	770 2	770 4
& Query	Match	100.0	9.66	99.6	99.6	99.6	9.66	99.2	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.6	98.4	98.3	98.2	98.2	98.2
	Score	1172	1167	1167	1167	1167	1167	1163	1156	1156	1156	1156	1156	1156	1156	1156	1156	1156	1156	1156	1156	1153	1152.5	1151	1151	1151
Result	No.	1	7	n	4	Ŋ	9	7	σ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aae15174 Human Sta	Add44740 Human Pro	Aay72851 Mouse Sta	Aay72847 Mouse Sta	Aay72854 Mouse Sta		Aay72848 Mouse Sta	Aay72852 Mouse Sta	Aay72849 Mouse Sta		Aay72844 Mouse Sta	Aaw62996 Human tru	Abu04748 Human exp	Adh57036 Truncated	Abr59713 Human sig	Aar72079 Human Sta	Aaw03170 Human STA	Aaw62995 Human Sta	Abu04747 Human exp	-
AAE15174	ADD44740	AAY72851	AAY72847	AAY72854	AAY72855	AAY72848	AAY72852	AAY72849	AAG78526	AAY72844	AAW62996	ABU04748	ADH57036	ABR59713	AAR72079	AAW03170	AAW62995	ABU04747	ABU04735
S	7	4	4	4	4	4	4	4	S	4	~	9	80	9	~	~	~	9	9
770	770	213	236	223	185	176	128	143	749	268	582	582	582	680	712	712	712	712	712
98.2	98.2	95.9	95.9	89.1	72.1	66.2	55.7	51.2	49.1	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8
1151	1151	1089	1089	1044	845	116	653	600	576	572	572	572	572	572	572	572	572	572	572
56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1

Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis; therapy; mutant; mutein. Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids) Location/Qualifiers AAY72862 standard; protein; 229 AA. (first entry) Misc-difference 19 Mus musculus. 31-MAY-2001 AAY72862; Key Region AAY72862 

/note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein" /note= "Wild type Leu substituted with Ala; corresponds to 148 position of Stat-3 protein" 213. .23 / note= "Stat3-c-Jum interaction region 2; corresponds to 342-358 position of Stat3 protein" WO200116605-A2 Region

30-AUG-2000; 2000WO-US023822. 99US-00387418. (UYRQ ) UNIV ROCKEFELLER. 31-AUG-1999; 08-MAR-2001.

Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein. WPI; 2001-226705/23.

Darnell JE;

Zhang X, Horvath C, Wrzeszcynska MH,

Claim 66; Page 85; 86pp; English.

The present sequence is mouse Stat3 mutant (1148A) protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .25
//note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein" 213. .229
//note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                 9
by replacing Leu 148 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat.3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse, Stat3 protein, transcription factor, c-Jun, gene transcription, cellular transformation, dysproliferative disease, cancer, psoriasis,
                                                                                                                                                                                                                                                                               1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                            100.0%; Score 1172; DB 4; Length 229; 100.0%; Pred. No. 1.2e-101; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Stat3 protein fragment #8 (130-358 amino acids).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 229; Conservative
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                                                                                                                                                                            Sequence 229 AA;
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is mouse Stat3 protein fragment containing 130-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of thysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                                                                                                 1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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/note= "Stat3-c-Jun interaction region 1;
130-154 position of Stat3 protein"
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/note= "Stat3-c-Jun interaction region 2;
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Stat3 protein fragment #4 (107-358 amino acids).
                                                                                                                                                                                                                                                                    Score 1167; DB 4;
Pred. No. 3.5e-101;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Darnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang X, Horvath C, Wrzeszcynska MH,
             Claim 65; Page 76-77; 86pp; English.
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Best Local Similarity
                                                                                                                                                                                                                                        Sequence 229 AA;
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27-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRRPEI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                The present sequence is mouse Stat3 protein fragment containing 107-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for treating cancer and psoriagis. A Stat protein comprises the N-terminal domain, colled-coil domain, but binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236. .252
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Stat3-c-Jun interaction region 1; corresponds 130-154 position of Stat3 protein"
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                                           Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                 99.6%; Score 1167; DB 4; Length 252; 99.6%; Pred. No. 4e-101; Live 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Stat3 protein fragment #2 (107-377 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                       Claim 65; Page 73; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY72841 standard; protein; 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2000; 2000WO-US023822
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                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 99.6
Matches 228; Conservative
              WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                     Sequence 252 AA;
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8 윤 ઠે 셤 ઠે 셤 ò 셤

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61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of Stat protein comprises and also for transing cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDFIVQHRPMLEERI 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                              Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.6%; Score 1167; DB 4; Length 271; 99.6%; Pred. No. 4.4e-101; ive 0; Mismatches 1; Indels (
                                                                              Darnell JE;
                                                                          Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                           Claim 65; Page 67-68; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR72082 standard; protein; 770 AA.
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93US-00126595
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Matches 228; Conservative
(UYRQ ) UNIV ROCKEFELLER
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                                                                              Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse Stat3 (19sf6).
                                                                                                                                                    WPI; 2001-226705/23
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NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1...25
/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"

    useful for diagnosing,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                            STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from splenic-fthymic cells. STAT4 includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery vides binding in a receptor-ligand specific manner. STAT proteins and the DNA binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and activation of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                              signal transducer and activator of transcription (STAT) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                   New STAT protein DNA-binding domain peptide(s) - useful for di
preventing or treating cellular dysfunction, e.g. oncogenesis,
inflammation, parasitic disease or autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.6%; Score 1167; DB 2;
99.6%; Pred. No. 1.8e-100;
iive 0; Mismatches 1;
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                                                                                                                                       Zhong
                                                                                                                                                                                                                                                                                                                    Disclosure; Page 87-90; 138pp; English.
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                                                                                                                                     Horvath CM,
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                  95WO-US017025.
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                                                                                               (UYRO ) UNIV ROCKEFELLER
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                                                                                                                                                                             WPI; 1996-333941/33.
N-PSDB; AAT31280.
                                                                                                                                       Wen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 770 AA;
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                  28-DEC-1995;
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                                                                                                                                       Darnell JE,
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                                                                                                                                                                                                                                                                                                                A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080) (Stat1) that was responsive to interferon- gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339 + Teceptor recognition factor proteins were isolated. The 2 genes (AAQ89339 + 40) were cloned in plasmids 138f1 and 138f6 and encoded proteins termed stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                 Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACIGGPPNICLDRIENWITSLABSQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , signal transducer and activator of transcription, protein, ligand, receptor, oncogenesis, inflammation, disease, antagonist, therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
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                                                                                                  7
                                                                                               Zhong
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Pred. No. 1.8e-100;
); Mismatches 1;
                                                                                                  'n,
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/label= DNA binding domain
/note= "Claim 3, page 110"
                                                                                                    Wen
                                                                                                                                                                                                                                                                                 Claim 1; Page 107-110; 160pp; English.
                                                                                                  Shuai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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94US-00212184
                94US-00212185
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                                                                                               Schindler CW,
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Best Local Similarity 99.6
Matches 228; Conservative
                                                          ROCKEFELLER
                                                                                                                                         1995-139598/18.
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                                                                                                                                                          N-PSDB; AAQ89340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 770 AA;
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                                                        (UYRQ ) UNIV
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11-MAR-1994;
                11-MAR-1994;
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                                                                                               Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse STAT4
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Best Local Similarity
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        Note= "Wild type Val substituted with Ala corresponds to 151 position of Stat-3 protein"
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                                                                                                                                                                                                                                                                                                                    containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing Val 151 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which medulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for medulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A
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                                  213. .229
/note= "Stat3-c-Jun interaction region 2; corresponds
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                      dysproliferative diseases and also for treating cancer and psoriasis. Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NHPTAAVVTEKQOMLEQHLODARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHPTAAVVTEKOOMLEOHAQDVRKRVODLEOKMKVVENLODDFDFDFNYKTLKSOGDMODLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                           present sequence is mouse Stat3 mutant (V151A) protein fragment
                                                                                                                                                                                                                                                 Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1163; DB 4; Length 229;
Pred. No. 8.3e-101;
0; Mismatches 2; Indels (
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                                                                                                                                                                                                   Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                   Claim 66; Page 86; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE22055 standard; protein; 720
                                                                                                                             30-AUG-2000; 2000WO-US023822
                                                                                                                                                    99US-00387418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.28;
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Best Local Similarity 99.1%;
Matches 227; Conservative
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                                                                                                                                                                            (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Stat3beta protein.
                                                                                                                                                                                                   Shang X, Horvath C,
                                                                                                                                                                                                                           WPI; 2001-226705/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 229 AA;
Misc-difference
                                                                               WO200116605-A2
                                                                                                                                                    31-AUG-1999;
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription of 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, mycoardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, coclusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, colliepsy, emphysema, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy citing and infamune response is useful for amplicating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, carthematosus, multiple sclerosis, insulin dependent diabetes mellitus, companients sprace of systemic polymyositis, chronic active hepatitis, anawamia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, anaemia, autoimmune charcipathy, autoimmune neutropenia, myasthenia gravis, allowed connective tissue disease, primary bilaary cirrhosis, myasthenia gravis, allowed connective theory and connective connective theory and connective connective anaemia, autoimmune charcipathy, autoimmune neutropenia, myasthenia gravis, allowed connective connective disease, primary bilaary cirrhosis, myasthenia gravis, allowed connective disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human
                                                     inflammation, chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; scleroderma; scleroderma; mitrogen cartive hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumacoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.
stroke; angiogenesis; myocardial infarction; hypoglycaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 87-89; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dalton W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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UNIV SOUTH FLORIDA.
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Score 1156; DB 5; Length 720; Pred. No. 1.8e-99;

98.6%;

Length 769;

Query Match

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conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB573702 to ABB57374) or by determining the protein sequences in ABB573702 to ABB57374) or by determining the expression profile of a gene group comprishing these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic condition improving drugs or therapeutics for sechaemic condition related sequence, which are used in the exemplification of the present invention
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ation or by
                                                                     NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
                                                                                                                                      190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEXVQKTLTDEELADWKRRQQI
                                                                                                                                                                                                      1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                      GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
                                                                                                                                                                             ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examining the ischemic condition (e.g. occlusive ischemia) by measur expression levels of particular genes defined in the specification of determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for examining ischaemic conditions, comprising measuring the average.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse ischaemic condition related protein sequence SEQ ID NO:398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease
Indels
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2;
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              ABB57164 standard; protein; 769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
Conservative
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Sequence 769 AA;

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                                                                                                 30 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                          180
                                                                                                                                                                                                                                      250 ACIGGPPNICLDRLENWITSLABSQLQTRQOIKKLBELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.
                                                                                                                                                                                                        ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                    1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                       GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEBLADWKRRPEI
                                                                                                                                                                       190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
                                  Gaps
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                                                                                                                                                                                                                                                                                              VELFRNIAMSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; signal transducer and activator of transcription
                                  7
Score 1156; DB 5;
Pred. No. 1.9e-99;
                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 83-85; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
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                                                                                                                                                                                                                                                                                                                                                                                                   AAE22054 standard; protein; 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-2000; 2000US-0231212P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-SEP-2001; 2001WO-US028254.
   98.6%;
98.7%;
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                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-362218/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Stat3 protein.
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                   Similarity
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                   Local Simi.
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Matches
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tischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, children adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, c.S. syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious maemia, autoimmune thyroiditis, idiopathic Addison's disease, viciligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, doodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and carcinoma edposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, ochon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative diseones and wounds. The present sequence is human Stat3 \$

Sequence 769 AA;

ö 189 120 249 180 1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN NHPTAAVVTEKQQMLEQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI Gaps .; 0 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229 310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358 98.6%; Score 1156; DB 5; Length 769; 98.7%; Pred. No. 1.9e-99; 1; Mismatches Matches 226; Conservative Best Local Similarity 61 190 181 Query Match g g 8 ò ò ò

RESULT 11 AAE22056

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AAE22056 standard; protein; 769 AA.

AAE22056; 

25-JUL-2002 (first entry)

Human protein related to angiogenesis regulation.

Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; theumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; disove's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.

Homo sapiens

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Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chicking, proliferative angiopathy e.g. diabetic microangiopathy with necvascularisation. Suppressing an immune response is useful for with necvascularisation. Suppressing an immune response is useful for with necvascularisation attoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, commercive tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, dispathic and such angential arribitis, dispathic Addison's disease, vitiligo, dispathic disease, rheumatoid arribitis, discoid lupus, ulcerative colitis and chease the method is useful in preventing or treating corrections corrections of preceding appoint provint and organic prolitis and corrections.
                                                                                                                                                                                                                                                                                                                                         Modulating anglogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human protein related to angiogenesis regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 83-85; 94pp; English.
                                                                                                                                                                                                                                                      Dalton W;
                                                                                                                                     08-SEP-2000; 2000US-0231212P.
                                                                                      10-SEP-2001; 2001WO-US028254
                                                                                                                                                                                                                                                      Jove R,
                                                                                                                                                                                                                                                                                                 WPI; 2002-362218/39
                                                                                                                                                                              (UY3C) UNIV JOHNS (UYSF-) UNIV SOUTH
                                                                                                                                                                                                                                                                                                                                                                                                                 of transcription 3.
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WO200220032-A1.
                                        14-MAR-2002.
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ö 121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180 NHPTAAVVTEKQOMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 60 130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI Gaps ö 98.6%; Score 1156; DB 5; Length 769; 98.7%; Pred. No. 1.9e-99; ive 1; Mismatches 2; Indels Matches 226; Conservative Local Similarity Query Match 셤 ð g 셤 ò ò

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AAR82995;

AAR82995

RESULT 12 AAR82995

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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. The encoding sequence differs from the original published human STAT3 gene sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3 protein er an be used for the recombinant expression of the variant. STAT3 protein is useful as a medicament or pharmaceutical composition for treatment of autoimmune or inflammatory diseases
                                                                                                                                                               Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNNÇSVTRÇKMQQLEQMLTALDQMRKSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human Signal Transducer and Activator of Transcription 3 (STAT3) allelic variant useful for treatment of autoimmune and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
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AAY03768 standard; protein; 770 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 9-13; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                 98EP-00102774.
                                                                                                                                                                                                                                                                                                                                                                                                                         97EP-00116061
                                                                                                                        Human STAT3 allelic variant
                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serlupi-Crescenzi O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-192664/17.
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                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1998;
                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1997;
                                                                                   11-JUN-1999
                                                                                                                                                                                                                                                                                                                                     31-MAR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIXKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                                                                 Mouse; acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                            Mouse liver acute phase response factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 20-22; 31pp; English.
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                                                               standard; protein; 770
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Best Local Similarity 98.7'
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kishimoto T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KISH/) KISHIMOTO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-346089/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nypertension, etc
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                                                                                                                                                                                                                                                                                                                      Mus musculus
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Akira S,

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Gaps

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RESULT 13

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Length 770;

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Signal transducer and activator of transcription; STAT3; drug development; drug discovery; crystal; inflammation; allergy; asthma; leukaemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity;
                                      250 ACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPWLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Conserved N-terminal domain of the STAT family"
                                                                                                   310 VELFRNIAMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKPPEL
                                                                                                                                                                                                                                                                                                                                                               viral disease; growth retardation; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                       AAE14652 standard; protein; 770 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-2000; 2000US-00556273.
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vinkemeier U, Moarefi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                    Murine STAT3 protein.
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                                                                                                                                                                                                                       AAE14652;
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Domain
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                                                                                                                                                                                                        The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than S.O Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for
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                                                             transducer and activator of transcription; crystal;
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/label= 3(10) helix of alpha helix 2

28...33

/label= Alpha helix 3

35...40

/label= Alpha helix 4

43...47

/label= Alpha helix 5
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                              N-terminal domain of murine STAT-3 protein.
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label= Alpha helix 1
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77. 96
/label= Alpha helix 7
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/label= Alpha helix 8
                                                                                                                                        ocation/Qualifiers
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08-NOV-2000 (first entry)
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Matches 226; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-505108/45.
                                                           STAT; signal transdu
drug design; murine.
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Kuriyan J;

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The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that binds to the N-terminal domain of a STAT protein, identifying a compound that enhances or diminishes the binding of the dimeric STAT proteins to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new cluds. An antagonist of STAT N-terminal dimeric interactions that inhibits the binding of the STAT dimers to adjacent weak binding sites on a promoter of a gene, could be useful as drugs in the treatment of diseases, e.g. inflammation, allery, asthma and leukaemias. On the other hand, an agonist of N-terminal dimeric interactions between STAT dimers,
      and activator of
new drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           can be used as drugs in the treatment of diseases e.g. anaemia, neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and growth retardation. The present sequence is murine STAT3 protein
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Identifying compounds that bind to signal transducer transcription proteins, useful for the production of
                                                                                                                                                                         Example; Col 47-50; 44pp; English.
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                                                            Best Local Similarity 98.7%; Pred. No. 1.9e-99;
Matches 226; Conservative 1; Mismatches 2; Indels
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Sequence 5, Al
Sequence 6, Al
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Compugen Ltd.
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US-08-369-796-12
US-08-852-091-12
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US-08-956-869-12
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US-09-364-970-3
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US-09-952-970-5
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US-09-972-800A-6
US-08-276-099A-14
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   version - 2005
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ALIGNMENTS

RESULT 1
US-09-387-418A-30
; Sequence 30, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT; Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-41BA-30

ö 120 180 9 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 1 NHPTAAVVTEKQOMLEQHAQDVRKRVQDLEQKMKVVENLODDFDFNYKTLKSOGDMODLN GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLAGLLSAMEYVQKTLTDEELADWKRRPEI ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI Gaps ö 229 Length 229; Score 1172; DB 3; Length; Pred. No. 1e-97; O; Mismatches O; Indels ccn 100.0%; al Similarity 100.0%; 229; Conservative 0. Query Match Best Local S Matches 229 61 61 121 121 셤 셤 g ð ð ઠે

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GENERAL INCORDATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: The Control of the Cont
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Pred. No. 3.6e-97;
                              181 VELFRNIMKSAFVVEROPCMPMHPDRPLVIKTGVOF
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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wzeseczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
TITLE OF INVENTION: METHODS FOR IDENTIFYING P
TITLE OF INVENTION: METHODS FOR IDENTIFYING P
TITLE OF INVENTION: METHODS FOR IDENTIFYING P
TITLE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILIGA DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATCHIN Ver. 2.0
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Best Local Similarity 99.6%;
Matches 228; Conservative (
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; ORGANISM: Mus musculus
US-09-387-418A-9
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Best Local Similarity
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SEQ ID NO 9
LENGTH: 271
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Parent No. 6331572
GENERAL INFORMATION:
APPLICANT: Shang, Xiaokui
APPLICANT: Wisesscrynska, Melissa H
APPLICANT: Wisesscrynska, Melissa H
APPLICANT: Darnell Jr., James B
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
FILE REFERENCE: 600-1-253
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
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Pred. No. 2.9e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
99.6%; Score 1167; DB 3;
Best Local Similarity 99.6%; Pred. No. 2.9e-97;
Matches 228; Conservative 0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
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Best Local Similarity 99.6
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Mus musculus
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Sequence 12, Application US/08852091
Patent No. 588328
GENERAL INFORMATION:
APPLICANT: 210ng Wen
APPLICANT: 2110ng Wen
TITLE OF INVENTION: FRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                        121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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Pred. No. 1.4e-96;
0; Mismatches 1;
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FILING DATE: 06-MAY-1997
CLASSIPRICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAMME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 Hackensack Avenue
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                             RESULT 7
US-08-852-091-12
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Patent No. 5716622

GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: APPLICANT: ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: FANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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                                                                                                                        GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                              24 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLN
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                                          1 NHPTAAVVTEKOOMLEOHAODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
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Pred. No. 1.4e-96;
0; Mismatches 1; Indels
  Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
  1,
  Mismatches
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.6
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-369-796-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                         181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                Sequence 12, Application US/08820754
; Patent No. 5976835
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong; Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; WUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.6%; Score 1167; DB 2; Length 770; 99.6%; Pred. No. 1.4e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUDNIERS: USA

CUDNIERS: USA

CUDNIERS: LODA

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOCTAMRE: Batentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 13-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
FILING DATE: 19-MAR-1993
FILING DATE: 19-MAR-1993
FILING DATE: 19-MAR-1993
FILING DATE: 24-SEP-1993
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESG., DAVIG A.
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INPORMATION:
TELEFRONSE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.46
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 770 amino acids amino acid
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Best Local Similarity 99.6
Matches 228; Conservative
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133521
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                       250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPWLEERI 309
190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEBLADWKRRPET
                                                                                                                                                                                                                                                                                                                                                                                   310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                                                      181 VELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Chindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: To Xian-Yuan
APPLICANT: Zhong, Zhong
ITILE OF INVENTION: RECEPTOR RECGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSE: Xiauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1167; DB 3; Length 770;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMINICATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 11-WAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-WAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-WAR-1993
PRIOR APPLICATION NUMBER: APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 12, Application US/08956652
; Patent No. 6013475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 770 amino acids
amino acid
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                           121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                       1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                        190 GNNQSVIRQKWQQLEQWLIALDQMRRSIVSELAGLLSAMEYVQKTLIDEELADWKRRPEI
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                                                                                                       Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08948547

Patent No. 6124118
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Pu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
ITILE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
ITILE OF INVENTION: SEQUENCES: 25
                                                                                                                                                        1; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
                                                                                                       Query Match 99.6%; Score 1167; DB 3; Best Local Similarity 99.6%; Pred. No. 1.4e-96; Matches 228; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PADLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-5EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA ZIP: 07601 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klauber & Jackson
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                               ; MOLECULE TYPE: protein US-08-956-869-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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STREET: 41:
          TOPOLOGY:
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US-08-948-547-12
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                                                                                                            130 NHPTAAVVTEKQQMLEQHLQDVRKKVQDLEQXMKVVENLQDDFDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                               61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                         250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                  9
                                                                                1 NHPTAAVVTEKOOMLEOHAQDVRKRVQDLEOKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                            121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
       Pred. No. 1.4e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PELLING DATA:

APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 08/126,588
FILING DATE: 24-SEP-1993
ATYONEY/AGENT INFORMATION:
NAME: Jackson Esq., 10-2013 CIP
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1897-5800
TELEFAX: 201343-1684
                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,869
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,185
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08956869
Patent No. 6030808
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STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
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INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
  99.68;
Best Local Similarity 99.6
Matches 228; Conservative
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US-08-956-869-12
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US-09-364-970-5
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Batent No. 6235873

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING FILE REFERENCE: 600-1-222

CURRENT APPLICATION NUMBER: US/09/364,970

CURRENT FILING DATE: 1999-07-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                  NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                       190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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Pred. No. 1.4e-96;
0; Mismatches 1; Indels (
                                                                                                                                                                                              Length 770;
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                                                                                                                                                                                                                                   Indels
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99.6%; Pred. No. 1.4e-96;
live 0; Mismatches 1;
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                                                                                    : 770 amino acide
amino acid
GY: linear
   201 487-5800
                                                                                                                                                                                          Query Match
Best Local Similarity 99.6
Matches 228; Conservative
                                TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.6
Matches 228; Conservative
                                                                     SEQUENCE CHARACTERISTICS
                  201 343-1684
                                                                                                                       ) TOPOLOGY: linear

// MOLECULE TYPE: protein

US-08-948-547-12
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TELEPHONE:
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                     TELEFAX:
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US-09-364-970-3
                                                                                    LENGTH:
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Sequence 5, Application US/09364970

Patent No. 6235873

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bromberg, Jacqueline

TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING

TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES

FILE REFERENCE: 600-1-252

CURRENT APPLICATION NUMBER: US/09/364,970

CURRENT APPLICATION NUMBER: US/09/364,970

WUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 770;
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APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1167; DB 3;
Pred. No. 1.4e-96;
0; Mismatches 1;
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APPLICATION NUMBER: US/08/956,653A
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APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 12, Application US/08956653A; Patent No. 6338949; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.6%;
                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.6
Matches 228; Conservative
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                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-5
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STATE: New Jersey
COINTRY: USA
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; Sequence 12, Application US/08212185
; Patent No. 6605442
; GENERAL INFORMATION:
APPLICANT: Darnell Jr., James B.
APPLICANT: Schindler, Christian W.
APPLICANT: Thus, Xian-Yuan
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: RECEPTOR SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
21P.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBCOMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY, AGENT INFORMATION:
NAME: Jackson Esq., David A.
RECISTRATION NUMBER: 26,742
REFERENCEY, DOWNER: 26,742
REFERENCEY, DOWNER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 99.6%
Matches 228, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 99.6%; Score 1167; DB 4; Length 770; Best Local Similarity 99.6%; Pred. No. 1.4e-96; Matches 228; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
  APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: 24-SEP-1993
NAME: JACKSON ESG., DAVID A.
UMBER: US/08/212,185
11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acide
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Search completed: May 25, 2005, 17:47:40 Job time : 29.6534 secs

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May 25, 2005, 17:36:58 ; Search time 100.287 Seconds (without alignments) 763.830 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1434725 seqs, 334507595 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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114:
114:
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                                                                                                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Appl	Appl	Appl	Appl	Appli	Appl	Appl	Appl	Appli	Appli	Appli	Appli	Appl
	30,	18,	28,	14,	, 6	12,	12,	31,	4,	2,	5, 7	8,7	56,
Description	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ai.	US-10-090-185-30	US-10-090-185-18	US-10-090-185-28	US-10-090-185-14	US-10-090-185-9	US-09-876-773-12	US-10-639-617-12	US-10-090-185-31	US-10-380-020-4	US-10-380-020-2	US-10-380-020-5	US-10-045-792-8	US-10-038-010-56
	13	13	13	13	13	11	11	13	15	15	15	14	14
* Query Match Length DB	229	229	229	252	271	770	770	229	720	169	169	770	770
* Query Match	100.0	9.66	9.66	9.66	9.66	9.66	9.66	99.2	98.6	98.6	98.6	98.6	98.6
Score	1172	1167	1167	1167	1167	1167	1167	1163	1156	1156	1156	1156	1156
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780, 780, 329, 349, 19,	Sequence 23, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 2, Appli	2, Apr 2, Apr 1, Apr 1, Apr 352, 7	Sequence 19, Appl Sequence 19, Appl Sequence 4, Appli Sequence 50, App Sequence 24, Appl Sequence 6, Appli Sequence 8, Appli
14 US-10-117-087-2 9 US-09-925-302-780 10 US-09-925-302-780 15 US-10-116-275-349 15 US-10-10-116-275-349 13 US-10-090-185-19 13 US-10-090-185-19 13 US-10-090-185-15	13 US-10-090-185-23 13 US-10-090-185-23 13 US-10-090-185-20 13 US-10-090-185-17 9 US-09-933-205-4 13 US-10-090-185-12 14 US-10-245-120-3 14 US-10-245-120-3 14 US-10-245-120-3	17 US-10-639-617-6 17 US-10-936-390-5 19 US-09-833-205-2 11 US-09-876-773-4 14 US-10-245-120-1 14 US-10-308-279-44 16 US-10-755-889-352 16 US-10-755-889-352	17 US-10-492-043-19 17 US-10-639-617-4 18 US-10-639-617-4 19 US-09-252-297-550 13 US-10-090-185-24 9 US-09-833-205-6 11 US-09-876-773-8
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114 114 118 118 118 118 118	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		) 4 4 4 4 4 0 4 5 6 6 6 0 1 5 6 6 7 6 6

# ALIGNMENTS

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APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzesczynska, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFRENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
NUMBER PATENTIN Ver. 2.0
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US-10-090-185-30; Sequence 30, Application US/10090185; Publication No. US20020197647A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus
US-10-090-185-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 30
LENGTH: 229
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Gaps

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Value 14. Application US/10090185

Sequence 14. Application US/10090185

Publication No. US2020197647A1

GENERAL INFORMATION:

APPLICANT: Chang, Xiaokui

APPLICANT: Arevath, Cut M

APPLICANT: Darnell Jr., James E

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-1-253

CURRENT APPLICATION NUMBER: US/10/090,185

CURRENT PILING DATE: 2002-03-04

FRIOR APPLICATION NUMBER: 09/387,418

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0
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                                                                          Length 229;
                                                                                                                      1; Indels
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                                                                        Score 1167; DB 13;
Pred. No. 6.4e-95;
                                                                                                                      0; Mismatches
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                                                                     99.6%;
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14
    ORGANISM: Mus musculus
                                                                     Query Match
Best Local Similarity
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                          US-10-090-185-28
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APPLICANT: Zhang, Xiaokui
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE OF INVENTION: INTERACTIONS
FILE OF INVENTION: INTERACTIONS
FILE OF INVENTION WHERE: US/10/090,185
CURRENT APPLICATION NUMBER: 09/387,418
PRIOR PILING DATE: 1999-08-31
NUMBER: OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhang, Xiaokui
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska,
APPLICANT: Horvath, Curt M
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT APPLICATION NUMBER: 09/387,418
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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  121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEBRI 180
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                                                                          181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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Pred. No. 6.4e-95;
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                                                                                                                                                                                                            Sequence 18, Application US/10090185; Publication No. US20020197647A1
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. Sequence 28. Application US/10090185
. Publication No. US20020197647A1
. GENERAL INFORMATION:
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Best Local Similarity 99.6%;
Matches 228; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVENTION: RECEPTOR RECOGNITION FACTORS,
                       FILING DATE: 11.MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 22-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/ACENT INFORMATION:
NAME: Jackson Esq., David A.
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , DB 11;
3e-94;
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Pred. No. 3e-94
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Darnell Jr., James E. Schindler, Christian Fu, Xian-Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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Matches 228; Conservative
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                                                                   APPLICANT: Zhang, Xiaokui
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Wizeszczynska, Melissa H
APPLICANT: Uservath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT PILING DATE: 2002-03-04
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLIDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 VELFRNIMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLVKFPEL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.6%; Score 1167; DB 13; Length 271; 99.6%; Pred. No. 7.9e-95;
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TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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REPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
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Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
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ADDRESSEE: Klauber & Jackson
Sequence 9, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.6
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Mus musculus
US-10-090-185-9
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US-09-876-773-12
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Sequence 4, Application US/10380020
| Sequence 4, Application US/10380020
| Publication No. US20040052762A1
| GENERAL INFORMATION:
| APPLICANT: Pardoll, Drew
| APPLICANT: Dalton, Willian
| TITLE OF INVERTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
| TITLE OF INVERTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
| CURRENT PAPLICATION NUMBER: US/10/380,020
| CURRENT FILING DATE: 2003-03-07
| PRIOR FILING DATE: 2000-09-08
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                                                                                                                        Length 229;
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Pred. No. 2.6e-93;
1; Mismatches 2;
                                                                                                                     Score 1163; DB 13;
Pred. No. 1.4e-94;
0; Mismatches 2;
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                                                                                                                     99.2%;
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SOFWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.74
Matches 226; Conservative
                                                                                                                           Query Match
Best Local Similarity 99.1
Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo Sapiens
                                      musculus
                                  ; ORGANISM: Mus
US-10-090-185-31
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US-10-380-020-2
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         TYPE: PRT
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Sequence 310
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Pred. No. 3e-94;
0; Mismatches 1;
                                                                                                                                                  APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO 083/02569
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: JGCKSON ESG., David A.
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTSICS:
LENGTH: 770 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201 343-1684
TELEX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity 99.6%;
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Best Local Similarity 99.6'
Matches 228; Conservative
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250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
    190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 249
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                                                   121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                                                                                                                                                                                                                                                                                                                                                                                          Moarefi, Ismail
Darnell, Jr., James B.
Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                            181 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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Pred. No. 2.9e-93;
1; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO SEQUENCE DESCRIPTION: SEQ ID NO: US-10-045-792-8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/10045792; Publication No. US20030003563A1; GENERAL INFORMATION: APPLICANT: Vinkemeier, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New Jersey
COUNTRY: USA
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Best Local Similarity 98.7°
Matches 226; Conservative
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APPLICANT: Pardoll, Drew
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: 2003-03-07
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 769
                                                             APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
TILLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFRENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT PILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                  98.6%; Score 1156; DB 15; Length 769;
98.7%; Pred. No. 2.8e-93:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.86
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/10380020 Publication No. US20040052762A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 98.7
nes 226; Conservative
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                            CRGANISM: Homo Sapiens US-10-380-020-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo Sapiens
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-380-020-5
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Matches
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; ORGANISM: Human
US-10-117-087-2
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US-09-925-302-780
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LENGTH: 793
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                                   250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 56, Application US/10038010
| Publication No. US20030040089A1
| GENERAL INFORMATION:
| APPLICANT: HYBRIGENICS |
| TILE REFERENCE: B4767A |
| CURRENT APPLICATION WUMBER: US/10/038,010 |
| CURRENT FILING DATE: 2002-07-23 |
| PRIOR APPLICATION NUMBER: US 60/259,377 |
| PRIOR PILING DATE: 2001-01-02 |
| NUMBER OF SEQ ID NOS: 67 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 56 |
| LENGTH: 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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Pred. No. 2.9e-93;
1; Mismatches 2; Indels 0
                                                                            181 VELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
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Publication No. US20030166854A1
GENERAL INFORMATION:
APPLICANT: BERLUPI-CRESCENZI, Ottaviano
APPLICANT: BERLUPI-CRESCENZI, Ottaviano
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
FILE REFERENCE: SERLUPI-Z
CURRENT APPLICATION NUMBER: US/10/117,087
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US/09/526,542
PRIOR FILING DATE: 2000-03-19
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: STAT3 : Transcription factor in LOCATION: (1)...(770) CTHER INFORMATION: US-10-038-010-56
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Best Local Similarity 98.7°
Matches 226; Conservative
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SEQ ID NO 2 LENGTH: 770 TYPE: PRT

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250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                                                                                  130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
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                                                                                                                                                                                                                                                                                    190 GNNQSVIRQKMQQLEQMLITALDQMRRSIVSELAGLLSAMBYVQKTLTDEELADWKRRQQI
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                                                                                                                             1 NHPTAAVVTEKOOMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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   Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 780, Application US/09925302
| Sequence 780, Application US/09925302
| Patent No. US20020044941A1
| CENERAL INPORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies |
| FILE REPERENCE: PA104
| CURRENT APPLICATION NUMBER: US/09/925,302
| CURRENT FILING DATE: 2001-08-10
| PRIOR PELING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR PLING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 8966
| SOFTWARE: Patentin Ver. 2.0
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Pred. No. 3e-93;
1; Mismatches 2; Indels
                                                                 Indels
Score 1156; DB 14;
Pred. No. 2.9e-93;
1; Mismatches 2;
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Job time : 101.62 secs
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   Query Match 98.6%;
Best Local Similarity 98.7%;
Matches 226; Conservative
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Best Local Similarity 98.7
Matches 226; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds (without alignments) 1019.898 Million cell updates/sec

US-10-090-185-30 1172 Perfect score:

1 NHPTAAVVTEKQOMLEQHAQ.....IKTGVQFTTKVRLLVKFPEL 229 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	ISGF3 p91-related	DNA-binding protei	interferon-depende	gamma-interferon a	interferon alpha-i	mammary gland fact		transcription acti	mammary gland fact	interleukin-4-indu	conserved hypothet	DNA-Binding Protei	tpr protein - huma	hypothetical prote		Ψ.	hypothetical prote		microtubule bindin	myosin heavy chain	>	364K Golgi complex	ro	dystrophin, muscle	kinesin-related pr	coiled coil protei	ody	MSP-300 protein -	
COTT VIEW TOO	ΩI	149508	A54444	A46159	A56047	A46160	I49274	S54772	G02317	S55527	A54740	A70387	157557	833124	G72593	T27075	AE1947	T24806	S51193	T13030	A59252	S21801	JC5837	T38077	A27605	A57107	T38435	533821	S30431	S43074
	DB	7	7	7	7	7	~	~	7	~	~	~	~	~	~	~	~	~	~	~	~	Н	7	~	-	Н	7	~	~	~
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de	Query Match	98.6	98.2	44.9	43.6	27.4	22.9	22.9	22.4	20.2	10.6	10.3	10.2	10.2	10.2	- 10.1	10.1	9.9	9.8	9.7	9.6	9.6		9.6	9.6	•	9.5	9.5	9.5	9.4
	Score	1156	1151	526.5	511	321	268.5	268.5	262.5	237	124.5	121	119.5	119.5	119	118.5	118.5	116	115	113.5	113	113	113	112.5	112	111.5	111.5	111.5	111.5	110.5
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myosin heavy chain	myosin heavy chain	myosin heavy chain	myosin heavy chain	hypothetical prote	myosin heavy chain	microtubule bindin	hypothetical prote	probable myosin he	SCP1 protein - rat	hypothetical prote	myosin heavy chain	myosin heavy chain	myosin heavy chain	nuclear/mitotic ap	Corrector median
806117	A33977	A47297	B43402	AC1814	A41604	H90279	T27055	F84730	S28061	AE2304	A27224	A59287	MWKW	T30336	3.50115
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### ALIGNMENTS

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C.Species: Mus musculus (house)
C.Species: Mus musculus (house)
C.Joace: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C.Accession: 149508; 149009
R.Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su Cell 77, 63-71, 1994
A.Title: Molecular cloning of APRF, a.novel IFN-stimulated gene factor 3 p91-related tr A.Title: Molecular cloning of APRF, a.novel IFN-stimulated gene factor 3 p91-related tr A.Accession: 149508
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Status: preliminary; tr
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-393, 'M',395-700,702-770 <RE2>
A,Residues: 1-393, 'M',395-700,702-770 <RE2>
C,Genetics: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890
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p91-related transcription factor - mouse
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RESULT 2 A54444 DNA-binding protein APRF - human

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A;Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; PID:g1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.B.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in
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A; Residues: 1-851 < YAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-748 <YAM>
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C;Species: Homo sapiens (man)
C;Date: 21-809-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kba ISGA;Reference number: A46159; MUID:92366557; PMID:1502203
                                          C;Accession: A54444

C;Accession: A54444

S;Niabilo, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud
Cell 77, 63-71, 1994

A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tra
A;Reference number: A54444; MUID:94208062; PMID:7512451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 ACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLEELHOKVSYKGDPIVQHRPMLEERI 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQOMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 60
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s: Homo sapiens (man)
21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                           A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:358950
A;Map position: 17q21-17q21
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor
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A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A
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                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-770 <RES>
A,Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                    A, Accession: A54444
A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1151; DB 2
Pred. No. 4e-69;
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A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
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98.3%;
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Best Local Similarity 46.24
Matches 104; Conservative
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Best Local Similarity 98.3
Matches 225; Conservative
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C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e. A;Reference number: A56047; MUID:94277038; PMID:8007943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P42228; GB:U09351; NID:9509502; PIDN:AAA19692.1; PID:950950
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein
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    --QVRQQLKKLEELEQKYTYEHDPITKNKQVLWDRTFSLF 298

                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 VTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 VTEKOOMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKS--QGDMQDLNGNNQS
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                                                                           185 RNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                              gamma-interferon activation site-binding protein Stat4 - mouse
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                                                                                                                       299 QQLIQSSFVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQEL
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43.6%; Score 511; DB 2;
Best Local Similarity 45.5%; Pred. No. 1.4e-26;
Matches 102; Conservative 48; Mismatches 66;
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250 GPPNACLDQLQ--
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A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:248538; NID:g758633; PIDN:CAA8 R;Liu, X.; Robinson, G.W.; Goullleux, F.; Groner, B.; Hennighausen, L. Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S54772; I49273

R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleuki
A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Accession: S54772
A;Accession: S54772
A;Accession: Speriminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-793 <MUI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 -----QSVTRQKMQQLEQML----TALDQMRRSIVSELAGLLSAMBYVQKTLTDEELA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 DWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 OWKRRQQIAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRAEHLCQQLPIPG-PVEEM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription activator stat5A - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: stat5 protein
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct.1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----QSVTRQKMQQLEQML----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWK
                                                                                                                                                                                                                                                                                                                                               194 POERMSRETALOOKOVSLETWLOREAQTLOOYRVELAEKHOKTLOLLRKOOTIILDDELI
                                                   AAVVTEKOOMLEOHAODVRKRVODLEOKMKVVENLODDFDFNY - KTLKSOGDMODLNGNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: U21103; NID: 9747971; PIDN: AAA80590.1; PID: 9747972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 LAEVNATITDIISALVTSTFIIEKQP------PQVLKTQTKFAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 LEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 RPMLEERIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 793;
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; Pred. No. 2e-10;
42; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-793 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.9%;
Best Local Similarity 30.6%;
Matches 70; Conservative 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mammary gland factor - mouse
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A. Residues: 1-786 <RES>
A. Cross-references: UNIPROT: P42232; UNIPROT: 09JKM1; EMBL: U21110; NID: 9747973; PIDN: AACS2 R; Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A. BRBO J. 14, 1166-1175, 1995
EMBO J. 14, 1166-1175
EMBO J. 14, 116
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A;Nolecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-432, E', 434-786 cMUJ-
A;Cross-references: EMBJ:248539; NID:9758635; PIDN:CAA88420.1; PID:9758636
R;Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris, BRBO J. 14, 1402-1411, 1995
A;Title: Interleukin-3 signals through multiple isoforms of Stat5.
A;Reference number: S54725; MUID:95246733; PMID:7537213
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(Species: Mus musculus (house mouse)
Cjate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
CjAccession: 149274; S54773; S54773; S54773; S6773; S6773; S7773; S7773; S7773; S7773; S7773; S7773; S7773; S7773; S7773; S7774; S77
                                              A;Accession: S53873
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Essidues: 1-196;392-591;684-730 <YAW>
A;Cross-references: EMBL:U18671
C;Genetics:
A;Genetics:
A;Genetics:
A;Antrons: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; C;Superfamily: human signal transducer and transcription activator STATSA
C;Keywords: signal transduction; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | | : | | | | : | | : | | : | | : | | DHGLEQLETWFTAGAKLLFHLRQLLKELKGLSCLVSYQDDPLTKGVDLRNAQVTELLQRL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 VTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVT 67
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A;Reference number: S53873; MUID:95192056; PMID:7885841
A;Accession: S53873
A;Status: nucleic acid seqüence not shown
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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conserved hypothetical protein aq_1006 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A70387
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A,Reference number: A70300, MUID:98196666; PMID:9537320

A,Rocession: A70387

A,Status: preliminary: nucleic acid sequence not shown; translation not shown

A,Molecule type: DNA

A,Residues: 1-978 < AQPS:

A,Cross-references: UNIPROT:067124; GB:AE000718; NID:g2983504; FIDN:AAC07092.1; FID:g298

A,Experimental source: strain VF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Accession: A54740
R, Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 EKQOMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQ 69
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C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032
                                                                                                                                                                                                                                                                                                                                                                  C.Species: Homo sapiens (man)
C.Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
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C,Superfamily: human signal transducer and transcription activator STAT5A
C,Keywords: DNA binding; transcription regulation
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                                                                                   224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
A;Accession: A54740; MUID:94367369; PMID:8085155
A;Accession: A54740; MUID:94367369; PMID:8085155
A;Accession: A54740; MUID:94367369; PMID:8085155
A;Molecule type: mRNA
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                                         176 LEERIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLV
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1 Similarity 23.3%; Pred. No. 1.7;
49; Conservative 38; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; Indels
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Pred. No. 0.82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POVLKTOTKFOAGVRFLL 297
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Best Local Similarity
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Best Local &
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                                                      Killn, J.

Submitted to the EMBL Data Library, December 1995

A;Reference number: H01043

A;Accession: G02317

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Residues: 1-794 <LIN>
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT: P42229; EMBL: U43185; NID: g1151169; PIDN: AAB06589.1; PID: g115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: 55527; 84433
R;Wakao, H.; Goullleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Atitle: Corrigionda. Mammary gland factor (MGF) is a novel member of the cytokine regula
A;Reference number: 555527; MUID:95188889; PMID:7882987
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A; Residues: 1-794 <WAK.
A; Cross-references: UNIPROT: P42231; EMBL: X78428; NID: 9602354; PIDN: CAA55191.1; PID: 96023
A; Note: this is a revision to the sequence from reference S44353
R; Wakao, H.; Gouilleux, F.; Groner, B.
BMBO J. 13, 2182-2191, 1994
A; Title: Manmary gland factor (WGF) is a novel member of the cytokine regulated transcri
A; Reference number: S44353; MUID: 94244619; PMID: 7514531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 RLSRETALQÓKQVSLÉAWLQREAQTLQÓYRVELAEKHQKTLQLLRKQÓTIILDDELIQWK 256
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C;Superfamily: human signal transducer and transcription activator STAT5A
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.4%; Score 262.5; DB 2; Length 794; Best Local Similarity 30.1%; Pred. No. 5.1e-10; Matches 69; Conservative 43; Mismatches 96; Indels 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 LEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLV
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A;Cross-references: EMBL:X78428
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Best Local Similarity
Matches 67; Conserv
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C; Accession: G02317
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Cippedies: Aeropyrum pernix
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Cipate: 20-Aug-1999 #text_change 09-Jul-2004
Cipate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Cipate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Cipate: 20-Aug-1999
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takai awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72593
A;Accession: G72593
A;Accute: preliminary
A;Residues: 1-533 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:Q9YCP2; DDBJ:AP000061; NID:g5104821; PIDN:BAA80205.1; PID:d
A;Experimental source: strain Kl
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :| | ::: :|: | : : :|: | 1387 ASLINNQNLIQVKKIGRRYKTQYE 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1447 ELKAQQDKVMETSAQSSGDHQE----QHVSVQEMQELKETLNQAETKSKSLESQ---- 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1497 --VENLOKTLSEKETEARNLOEOTVOLOSE----LSRLRODLODRTTOEEOLROOITEKE 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 SAMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 MSQQLQALAEDLESLSSRVEDLEARVGSVEDRLSQAEEDIDSLTTSLDSLRTELEDLSTR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 TLKSQ------GDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLL 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -RVQDLEQKMKV---VENLQDDFDFNYK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; PID:g1296798
C;Genetics:
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A; Molecule type: mRNA <MI2>
A; Residues: 1-725, L'.
A; Residues: 1-725, L'.
A; Cross-references: ENBL: X63105; NID: 937257; PIDN: CAA44819.1; PID: 937258
R; King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
A; King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
A; Title: Tpr homologues activate met and raf.
A; Reference number: 800928; MUID: 88262257; PMID: 3387099
                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-31, "K', 33-142 < KIN>
A; Cross-references: EMBL: Y00672; NID: g37255; PIDN: CAA68681.1; PID: g37256
R; Greco, A.
Submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
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1551 EKTRKAIVAAKSKIAHLAGVKDQLTKENEELKQRNGALDQQ 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 ELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 VTEKQQMLEQHAQDVRKRVQDLEQKMKVVEN----LQDDF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
10.2%; Score 119.5; D
Best Local Similarity 20.4%; Pred. No. 5.1;
Matches 45; Conservative 50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GDB:128821; OMIM:189940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Scatus: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 144-228 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AVVTEKQQMLEQHAQDVRK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: H00592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1q25-1q25
A; Introns: 177/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 41; Conserva
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                                                                                                                                                                                                                                                                               A; Accession: S00928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB: TPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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C; Date: 22-Nov-1993 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C; Accession: S3124; S23740; S 50928; G01185
R; Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 2329-2333, 1992
A; Title: The human typ: gene encodes a protein of 2094 amino acids that has extensive coin A; Reference number: S33124; MUID:93064711; PMID:1437155
A; Accession: S33124
A; Reference number: S33124; MUID:93064711; PMID:1437155
A; Accession: S33124
A; Residues: 1-2094 cMIT>
A; Residues: 1-2094 cMIT>
A; Residues: 1-2094 cMIT>
A; Residues: 1-2094 cMIT>
A; Cooper, C.S.
Oncogene 7, 383-388, 1992
A; Title: Nucleotide sequence analysis of human tyr cDNA clones.
A; Reference number: S23740; MUID:92195670; PMID:1549355
A; Accession: S23740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CiAccession: 157557
Riguelle, Fw.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Cleve Riguelle, Fw.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Cleve Mol. Cell. Biol. 15, 3336-3343, 1995
Aprices of murine State and human State, Stat proteins that are tyrosine phosph A; Reference number: 157557; MUID:95280934; PMID:7760829
Aprocession: 157557
Aprices of murine State from GB/EWBL/DDBJ
Aprices of preliminary; translated from GB/EWBL/DDBJ
Aprices: Thin arm and Translated from GB/EWBL/DDBJ
Aprices of mRNA
Aprices of MUID:952633; GB:L47650; NID:91008876; PIDN:AAA79006.1; PID:910088
C;Genetics:
Aprice of MUID:952633; GB:L47650; MID:91008876; PIDN:AAA79006.1; PID:910088
C;Genetics:
Aprice of MUID:91008876; PIDN:AAA79006.1; PID:91008876; PIDN:AAA79006.1; PIDN:AAA79006.1; PIDN:AAAA79006.1; PIDN:AAAA79006.1; PIDN:AAAA7900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                   253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 D-----LNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDEELA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 NLIDPPLNGPGPS-----EDLPTILQ------GTVGDLETTQ-PLVLLRIQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 DWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLE-ELQQKVSYKGDPIVQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I57557
                                       WKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                           174 PMLEERIVELFRN-----LMKSAFVVERQ 197
                                                                                                                                                                                                                                                                   394 EEKLEKIKELFSEEEYTSLKMKERLLVELQ 423
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Best Local Similarity
Matches 60; Conserv.
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A.Gene: CESP:Y51A2D.16
A.Map position: 5
A.Introns: 17/3; 45/1; 76/2; 156/3; 240/2; 288/2; 594/2; 657/3; 756/3; 798/2; 900/3; 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1166 <WIL>
A;Cross-references: EMBL:AL021497; PIDN:CAA16403.1; GSPDB:GN00023; CESP:Y51A2D.16
A;Experimental source: clone Y51A2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                              : || ::| :: | :: | 490 NDLKTCQTQLELES------KKLQRLREDLVLEKSRRADLIGRIHSLCTTLSLNGA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540 NFEKINNDBELIDNIDDIMMAALVAVKRERDDIRIQGNQQIQELHDLKRDIEKLRRSESE 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600 SLNESDDRVRELTRENMHTKEQVFMLQEKLRELNLELSTKNDEI----DMVKASIEELNR 655
49 TLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTD 108
                                                                                             109 BELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQ----TRQQIKKLEELQQKVSY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 FNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEY--- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 CLDRLENWITSLAESQLQTRQQI----KKLEELQQKVSYKGDPIVQHRPMLEERIVELFR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NHPTAAVVTEKQ----QMLEQHAQ-----DVRKRVQDLEQKMKVVENLQDDFD 44
                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Y51A2D.16 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 -VQKTLTDEELAD-------WKRRPEIACIGGPPNI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75; Indels 69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;McMurray, A. submitted to the EMBL Data Library, January 1998 submitted to the EMBL Data Library, January 1998 streference number: 220307 streference number: 27075 streference in T27075 streference preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
10.1%; Score 118.5; I
Best Local Similarity 20.7%; Pred. No. 3;
Matches 50; Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: May 25, 2005, 17:45:29
Job time : 22.6038 secs
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-----ELRTQLDEKTRE 497
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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 95.284 Seconds

(without alignments)

1230.701 Million cell updates/sec
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Title: US-10-090-185-30 Perfect score: 1172 Sequence: 1 NHPTAAVVTEKQQMLEQHAQ......IKTGVQFTTKVRLLVKFPEL 229

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt\_03:\*
 1: uniprot\_sprot:\*
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		sapien	sculu	norv	nrus	gall	s lae	s lae	danio	s lat	s lat	danio	danio	don f	ynchu	mula	s lae	norv	norv	sculu	musculu .	musculu	musculu	sculu	apien	sapien	scrofa	musculu	ynchu	danio	danio	danio
	ption	homo s	mus musculu	rattus norv	bos taurus	gallus gall	xenopus	xenopus	brachydanio	oryzias la	oryzias lat		brachydanio	tetraodon f	oncorhynchu	macaca mula	xenòpus lae	rattus norv	rattus norv	mus musculu	mus mu	mus mu	արթ ար	mus, musculu	homo sapien	homo sa	BUB BC	mus mus	oncorhynchu	brachydanio	brachydanio	brachydanio
	Description	P40763	P42227	P52631	P61635	06dv79	09pvx8	Q7zxk3	Q7zt85	Q6dv£3	Qégue 7	Q6nv46	093599	Q90y16	013133	Q9n145	08jgn0	Q6p6q7	09qxk0	Q8C497	Q99k94	Q8c3v4	Q9d323	Q8c8m3	P42224	00P89Ö	Q764m5	P42225	013131	093598	Q6p943	08 j fu8
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SUMMARIES	ΙD	STA3 HUMAN	STA3 MOUSE	STA3 RAT	STA3 BOVIN	06DV79	Q9PVX8	Q7ZXK3	Q7ZTS5	Q6DVF3	Q6GUE7	Q6NV46	093599	Q90Y16	013133	Q9N145	Q8JGN0	Q6P6Q7	Q9QXK0	Q8C497	Q99K94	Q8C3V4	Q9D323	QBCBM3	STA1 HUMAN	0 <u>0</u> 0890	Q764M5	STA1 MOUSE	013131	093598	Q6P943	QBJFU8
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	Query Match Length	770	770	770	770	771	769	166	414	765	785	786	806	764	767	163	751	712	749	749	712	749	749	755	750	750	757	749	754	749	749	528
de	Query Match	98.6	98.6	98.4	98.0	96.5	93.7	93.4	86.2	86.2	86.2	86.2	86.2	84.1	83.3	56.0	49.3	49.1	49.1	49.0	48.9	48.9	48.9	48.9	48.8	48.8	48.8	48.2	46.2	45.6	45.6	45.6
	Score	1156	1156	1153	1149	1131	1098	1095	1010	1010	1010	1010	1010	986	916	929	578	576	576	574	573	573	573	573	572	572	572	565	541.5	535	535	534
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Q704w6 bos taurus			Q90y17 tetraodon f	•	_		Q7zz53 brachydanio			Q8jfu7 brachydanio	_	_	Q90y15 tetraodon f
		3				ĕ							
Q704W6	Q801Y2	STA4 HUMA	Q90YI7	013132	Q8AW24	STA4 MOUS	Q7ZZ53	Q8AW20	Q72277	Q8JFU7	Q66HB2	Q8JFS5	Q90Y15
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45.4				518.5 44.2				43.3		.2	43.2	_	494 42.2

# ALIGNMENTS

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### STOCKED STANDARD;

### STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11773079; DOI=10.1074/jbc.M111486200;
PubMed=11773079; DOI=10.1074/jbc.M111486200;
Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
Giraud S., Einverion of STAT3 transcription factor with the coactivator NcoA/SRC1a.";
J. Biol. Chem. 277:8064-8011(2002).
-!- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acute-phase protein genes.
--- PATHWAY: Involved in the gpl30-mediated signaling pathway.
--- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI.
--- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Del-701;
Isold=P40763-2; Sequence=VSP 010474;
-:- TISSUE SPECIFICITY: Heart, braIn, placenta, lung, liver, skeletal muscle, kidney and pancreas.
-:- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.
-:- SIMILARITY: Belongs to the transcription factor STAT family.
-:- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                             PHOSPHORYLATION ON SERINE.
MEDLINE=55215643; PubMed=7701321;
Stang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
"Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                 ·.
                                                                                                                                                                                                                               Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P40763-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in response to phosphorylation. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ012463; CAA10032.1; -. AY572796; AAS66986.1; -. BC000627; AAH00627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC014482; AAH14482.1; -. EMBL; AF029311; AAB84254.1; -.
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                                                                                                                                                                                          SEQUENCE OF 564-704 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                Science 267:1990-1994(1995).
                                                                                                                            and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:11364; STAT3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reansfac; T01493; -.
                                                                                                                                                                                                                TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P42227
                                                                                                                                                                                                                                                                                                                                                                                   complexes."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKALEELQQKVSYKGDPIVQHRPWLEERI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NHPTAAVVTEKOOMLEOHAODVRKRVODLEOKWKVVENLODDFDFNYKTLKSOGDMQDLN 60
GO; GO:0003700; F:transcription factor activity; TAS.
GO; GO:0006928; P:cell motility; TAS.
GO; GO:0007259; P:JAK-STAT cascade; TAS.
GO; GO:0001259; P:JAK-STAT cascade; TAS.
GO; GO:0001259; P:GAT cascade; TAS.
GO; GO:0007165; P:Signal transduction; TAS.
R GO; GO:0007165; P:Signal transduction; TAS.
R InterPro; IPR0009867; FB2.
R InterPro; IPR0009867; FB2.
R InterPro; IPR0009867; FB2.
R InterPro; IPR001217; STAT.
R Ffam; PF00117; STAT.
R Ffam; PF02117; STAT.
R Ffam; PF02118; PS0011; STAT.
R Ffam; PF02118; PS0011; STAT.
R PACITIE; PS0001; STAT.
R PACITIES PS0001; STAT.
R PACIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
                                                                                                                                                                                                                                                                                                                                                                                              Phosphotyrosine (by JAK) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.6%; Score 1156; DB 1; Length 770; 98.7%; Pred. No. 3.1e-65; ive 1; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphoserine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform Del-701)
/FIId=VSP_010474.
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T -> A (in Ref. 1).
6C00632211C8012D CRC64;
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/FIId=VAR_018683.
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P -> S (in Ref. 1).
K -> N (in Ref. 1).
F -> Y (in Ref. 1).
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/FTId=VAR
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Name=Stat3; Synonyms=Aprf;
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Matches 226; Conservative
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460 4
548 5
561 5
667 6
730 7
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AC P42227;
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CETRAINE-EVBN/N; TISSUE-Mammary gland;

MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MAIschul S.F., Zeeberg B., Barchow K.H., Schaefer C.F., Bhat N.K.,

MAIschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

MA Stapleton M., Judin T.B., Toshiyuki S., Carninci P., Prange C.,

MA S.A., McEwan P.J., McKernan K.J., Male M.A., Gay L.J., Hulyk S.W.,

MA S.A., McEwan P.J., McKernan K.J., Male M.J., Gay L.J., Hulyk S.W.,

MILIAON D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Radesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Matting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Matterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

M. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95014185; PubMed=7523373;
Raz R., Durbin J.E., Levy D.E.;
"Acute phase response factor and additional members of the interferonstimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
                                                                                                                                                                                                                 Zhong Z., Wen Z., Darnell J.E. Jr.;
"Stat3: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6.";
Science 264:95-98(1994).
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T.; "Molecular cloning of ARRF, a novel IRN-stimulated gene factor 3 p91-related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and CS7BL/6; TISSUE=Liver;
MEDLINE=96016116; PubMed=780809;
Schaefer T.S., Sanders L.K., Nathans D.;
"Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pubmed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.;
"Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/6J, and NOD/LtJ;
Davoodi-Semiromi A., She J.-X.;
Am mutant StatSb with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM STAT3A).
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                                                                                                                                                                                             MEDLINE=94188718; PubMed=8140422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 71:150-155(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zebrafish to mouse."
                                                                                                        Cell 77:63-71(1994).
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                                                                                           pathway
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PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                   (IL-6) responsive elements identified in the promoters of various acute-phase protein genes. STAT3B interacts with the N-terminal part of JUN to activate such promoters in a cooperative way.

-!- PATHWAY: Involved in the gp130-mediated signaling pathway.
-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).
-!- SUBCELULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.
MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9; Wen Z., Zhong Z., Darnell J.E., Jr., Wen Z., activation of transcription by Statl and Stat3 requires both tyrosine and serine phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and Kidney. STAT3B is also detected in the liver, although in a much less abundant manner.

FYAT3B TAYS IN A STAT3B is also detected in the liver, although in a much less abundant manner.

FYAT3B TAYS IN A STAT3B IS IN A STATAB IS IN A STATABLE AND A STATAB IS IN A STATABLE AND A STATAB IS IN A STATABLE AND 
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                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
MEDLINE-98334373; PubMed=9671298; DOI=10.1038/28101;
BECKET S., GYONET B., Mueller C.W.;
"Three-dimensional structure of the Stat3beta homodimer bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pro.
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GG; GO:0005737; C:cytcplasm; IDA.
GG; GO:0005634; C:nucleus; IDA.
GG; GO:000588; C:plasma membrane; IDA.
GG; GO:0005815; F:DNA binding; IDA.
GG; GG:0005515; F:protein binding; IDA.
GG; GG:0005515; F:transcriptional activator activity; IDA.
GG; GG:0007259; F:transcriptional activator activity; IDA.
GG; GG:0007557; P:regulation of transcription from Pol II F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Stat3B;
IsoId=P42227-2; Sequence=VSP_006287;
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InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2, 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT_bind; 1.
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EMBL; U06922; AAA19452.1; --
EMBL; U08378; AAA19458.1; --
EMBL; U08378; AAA56668.1; --
EMBL; AY29489; AAC52612.1; --
EMBL; AY29489; AAC57418.1; --
EMBL; AY29489; AAC75419.1; --
EMBL; AY29490; AAC75419.1; --
EMBL; BC003806; AAH03806.1; --
PIR; 149508; 149508.
PDB; 1BG1; X-ray; A=1-722.
TRANSPAC; T01574; --
MGD; MG1:103038; Stat3.
                                                                                                                                                                                                                                                                                                                                                Nature 394:145-151 (1998)
                                                                                                                                Cell 82:241-250(1995)
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                                                                                                                      Phosphoserine.
TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
                                                                                                     (By similarity).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                     /FTIC=VSP 006287.
Missing (In isoform Del-701).
/FTIC=VSP_010475.
S->A: Decreased transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 770;
Pfam, PF02865; STAT int; 1.
SNOSITE, PS5001; SHZ; 1.
3D-structure; Activator; Acute phase; Alternative splicing;
Direct protein sequencing; DNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                            E -> K (in Ref. 2).
S -> T (in Ref. 2 and 4).
M -> I (in Ref. 1).
                                                                                                       Phosphotyrosine (by JAK)
                                                                 Phosphorylation; SH2 domain; Transcription regulation.
DOWAIN
SH2.
MOD_RES 705 705 Phosphotyrosine (by JAK)
MOD_RES 727 Phosphoterine.
VARSPLIC 716 770 TTCSNTIDLPMSPRTLDSLMQFGNN
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01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.6%; Score 1156; DB 1;
ilarity 98.7%; Pred. No. 3.1e-65;
Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                activation.
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Rattus norvegicus (Rat).
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253
290
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nes 226; Conserv
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Matches
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                                                                                                                                                                                                 The elements.";
J. Biol. Chem. 270:29998-30006(1995).

J. Biol. Chem. 270:29998-30006(1995).

L. PUNCTION: Transcription factor that binds to the interleukin-6 (Li-6)-responsive elements identified in the promoters of various acute-phase protein genes.

C. I. PATHWAY: Involved in the gpl30-mediated signaling pathway.

C. I. SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI (By similarity).

C. I. SUBCELDIAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).

C. I. PIM: Tyrosine phosphorylation (By similarity).

C. I. FIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 thomodimers and maximal transcriptional activity (By similarity).

C. III, SIMILARITY: Belongs to the transcription factor STAT family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
                                                                                                                   "Transcription factors Stat3 and Stat5b are present in rat liver nuclei late in an acute phase response and bind interleukin-6 response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865, STAT bind; 1.
SMART; SM0252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998; Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.4%; Score 1153; DB 1; Length 770; 98.3%; Pred. No. 4.8e-65; 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphotyrosine (by JAK) (By
Phosphoserine (By similarity)
D74AOC76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X91810; CAA62920.1; -.
HSSP; P4227; 1BG1.
RGD; 3772; Stat3.
InterPro; IPR008967; P53_like_DNA_bnd.
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        770 AA; 88039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation.
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Name=stat 3;
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PROSITE; E
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9PVX8;
                                                                                                                                                                                 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stat 3.
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Q9PVX8
DE PER LA PERPLETA LA PER LA P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                           TISSUB-Mammary gland;

A Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;

Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;

The STATS-encoding gene was flipped across the STAT3/STAT5A-locus
T during ruminant evolution.";

Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Transcription factor that binds to the interleukin-6

(IL-6) -responsive elements identified in the promoters of various acute-phase protein gene (By similarity).

-!- PATHWAY: Involved in the gpl30-mediated signaling pathway.

-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).

-!- SIMILARITY: Belongs to the transcription factor STAT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GNNOSVTROKMOQLEOMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309
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PROSITE; BS251001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphotyrosine (by JAK) (By similarity)
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                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphoserine (By similarity)
9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                           05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 8.6e-65;
1; Mismatches 3
                     770 AA.
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 770 AA; 87974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 98.3%;
les 225; Conservative
                     STANDARD;
                                                                                                                                                                                                    Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                 Bovinae; Bos
                     BOVIN
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MOD_RES
SEQUENCE
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Matches
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771 AA

PRT;

PRELIMINARY;

Q6DV79 Q6DV79;

RESULT 5 **06DV79** 

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131 HPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLNG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 NNQSVTRQKMQQLEQMLTALDQMRRGIVSELAGLLSAMEYVQKMLADEELADWKRRQQIA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 CIGGPPNICLDRLENWITSLABSQLQTRQQIKKLEBLQQKVSYKGDPIVQHRPMLBERIV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 CIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIV 181
                                                                                                                                                                                                                                                14. SEQUENCE FROM N.A.

15. Zhou G.Y., Leung F.C.;

16. Zhou G.Y., Leung F.C.;

17. Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

18. Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

18. FWBL; AY641397; AA764897.1; -

18. GO; GO:0005634; C:nucleus; IEA.

18. GO; GO:000417; F:signal transducer activity; IEA.

18. GO; GO:0007242; P:intracellular signaling cascade, IEA.

19. GO; GO:0007242; P:regulation of transcription, DNA-dependent; IEA.

19. GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

19. InterPro; IPR000980; SH2.

19. RinerPro; IPR001217; STAT.

19. Ffam; PF001017; STAT alpha; 1.

19. Ffam; PF01017; STAT alpha; 1.

19. Pfam; PF02864; STAT alpha; 1.

19. Pfam; PF02865; STAT int; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNG
                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
Nishinakamura R., Mateumoto Y., Matsuda T., Ariizumi T., Heike T.,
Asashima M., Yokota T.;
"Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus embryos independent of BMP-4.";
Dev. Biol. 216:481-490(1999).
EMBL; AB017701; BAA66061.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
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                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                 Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1131; DB 2;
Pred. No. 1.2e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     769 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.5%;
25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50001; SHZ
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                       NCBI_TaxID=9031;
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'Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VELFRNIAMSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                    TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO44717; AAH44717.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87599 MW; 31018A3321CCEB9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 1095; DB 2; ]; Pred. No. 2.3e-61; 11; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.4%;
91.7%;
                                                                                                                                                                                                             Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, Stat3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.74
Matches 210; Conservative
                  mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              766 AA;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                             initiative.
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MEDINE=22388257, PubMéd=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Habeh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Warnsina K., Farmer A.A., Rubin G.M., Hong L.,
Bronstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A.,
Nhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                            1 NHPTAAVVTEKOOMLEOHAODVRKRVODLEOKWKVVENLODDFDFNYKTLKSOGDMODLN
                                                                                                                                                                                                                                                                                                                                                                                                                                               130 SHPNAAVVTEKOOMLEQHLODVRKKVODLEOKMKVVENLODDFDFNYKTLKSOSDLSELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                       Gaps
          GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; FS3 like_DNA_bnd.
InterPro; IPR00980; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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                                                                                                                                                                                                                                                                                                                           Score 1098; DB 2; Length 769;
Pred. No. 1.5e-61;
9; Mismatches 8; Indels C
                                                                                                                                                                                                                                                                      50001; SH2; 1.
769 AA; 87974 MW; 0905C03263303069 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                    Pfam; PF00017; SH2; 1.

Pfam; PF010107; STAT alpha; 1.

Pfam; PF02864; STAT bind; 1.

Pfam; PF02865; STAT_intt; 1.

PROSITE; SM02522; SH2; 1.

PROSITE; PS50001; SH2; 1.

SEQUENCE 769 AA; 87974 MW;
                                                                                                                                                                                                                                                                                                                               93.7%;
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                 Similarity
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Matches 212;
                                                                                                                                                                                                                                                                                                                               Query Match
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310 SHPNAAVITEKQQMLEQHLQDVRKKVQDLEQKMKVVENLQDDFDFNYKTLKSQSDLSELN 189 120 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI ACIGGPPNICLDRLENWITSLAESQLQTRQQIRKLEELQQKVSYKGDPIVQHRPMLEERI 1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0004871; F:signal transducer activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

R GO; GO:0007342; P:intracellular signaling cascade; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR000980; SH2.

R InterPro; IPR000980; SH2.

R Pfam; PF001017; SH3.

R Pfam; PF001017; SH3.

R Pfam; PF02864; STAT alpha; 1.

R Pfam; PF02864; STAT alpha; 1.

R Pfam; PF02865; STAT int; 1.

R SWART; SW00252; SH2; 1.

R PROSITE; PS50001; SH2; 1. Gaps Brachydanio rerio (Zebrafish) (Danio rerio) Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio. MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; Genetic and genomic tools for Xenopus research: The NIH Xenopus ; VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTNKVRLLVKFPEL 358

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us-10-090-185-30.rup

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NCBI_TaxID=8090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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             SON THE PROPERTY OF THE PROPER
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alteshul S.F., Zeeberg B., Wagner L., Schaefer C.F., Bhat N.K.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Aptischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Aptischul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Anilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Multing M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
And Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Alones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 HPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004871; F:signal transducer activity; IEA.

GO; GO:0004871; F:transcription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR008367; PS3 like_DNA_bnd.

InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation factor 3.
25-OCT-2004 (Medaka fish) (Japanese ricefish).
26-OCT-2004 (Medaka fish) (Japanese ricefish).
27-OCT-2004 (Medaka fish) (Japanese ricefish).
28-OCT-2004 (Medaka fish) (Japanese ricefish).
28-OCT-2004 (TrEMBLrel) (Japanese ricefish).
28-OCT-2004 (TrEMBLrel) (Japanese ricefish).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC045276; AAH45276.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF02865; STAT_int; 1.
PF02865; STAT_int; 1.
a14 AA; 48253 MW; OFFD1B509B7526BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 194; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               765 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZDB-GENE-980526-68; stat3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF01017; STAT alpha; 1.
PF02864; STAT bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P42227; 1BG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIKKLEELQQKVSYKGDPIIQHRPALEEK 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 HPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
SiJUL-2004 (Medaka fish) (Japanese ricefish)
Cryzias latipes (Medaka fish) (Japanese ricefish)
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY641434, AAT46364.1;
EMBL, AY641434, AAT46364.1;
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:000470; F:transcription factor activity; IEA.
GO; GO:0005724; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009896; P53 like DNA bnd.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                               Submitted (WAY-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; AR239947; AAT64912.11 -.
GO; GO:0005634; C:nucleus; IRA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; PSJ like_DNA_bnd.
InterPro; IPR00980; STAT.
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Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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84.3%; Pred. No. 5.6e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00017; SHZ; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT_int; 1.
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Pfam; PF01017; STAT_alpha; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 194; Conservative
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                                                                                                                                               SEQUENCE FROM N.A.
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Query Match
Best Local Similarity
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RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Braheton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Braha S.B., Loquellano N.R., Peters G.J., Abrameon R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,
Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raheley J., Helton E., Ketteman M., Radan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S.J., Marra M.A.;
R "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                          120 JACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                        GNNQ-SVTROKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
                                                                                                                             9
                                                                                                                          2 HPTAAVVTEKOOMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                                   Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                              310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTNKVRLLVKFPEL 359
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2
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                                                                   86.2%; Score 1010; DB 2; Length 785; 84.3%; Pred. No. 5.7e-56; Live 20; Mismatches 14; Indels
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Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC064320; AAH68320.1; -.
ZFIN; ZDB-GENE-980526-68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
           Pfam; PF02865; STAT_int; 1.*
PROSITE; PS50001; SH2; 1.
SEQUENCE 785 AA; 89643 MW; 81F231BDE27DE938 CRC64;
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Last annotation update)
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Pfam; PF02864; STAT_bind; 1.
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                                                                              Best Local Similarity 84.3%
Matches 194; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stat3 protein.
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The GO, GO:0006834; Crincleus; IEA.
The GO; GO:0006834; Crincleus; IEA.
The GO; GO:0006835; Printracellular signaling cascade; IEA.
TherPro; IPR0008967; PS3 like_DNA_bnd.
TherPro; IPR000980; SH2.
TherPro; IPR0017; SH2.
The Pfam; PF0017; SH2.
The Pfam; PF0017; SH2.
The Pfam; PF0017; SH2.
The Pfam; PF001864; SH2.
The Pfam; PF001864; SH2.
The Pfam; PF001865; SH2 like.
The Pfam; PF001865; SH3 like.
The Pfam; PF001866; SH3 like.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxIb=7955;
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0005155; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00980; SH2.
InterPro; IPR00117; SH2.
InterPro; IPR00117; SH2.
Pfam; PF00107; SH2; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_bind; 1.
Pfam; PF02865; STAT_bind; 1.
PROSTIE: PS05001; SH2.
SEQUENCE 786 AA, 90039 MW; PC7371D0B0E5447E CRC64;
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; 92151 MW; 74BC4EA401C3C942 CRC64;
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Last sequence update)
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Pred. No. 5.9e-56;
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01-NOV-1998 (TrEMBLrel. 08,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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01-JUL-1997
01-JUL-1997
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                                                                              120 JACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                 250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPIIQHRPALEEK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IACIGGPPNICLDRLETWITSLAESQLQIRQQIKKLEELQQKVSYKGDFIIQHRPALEEK 309
                                                                  GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                     2 HPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 HPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSF; F42C.7, LOUGHOUS; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000742; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
Pfam; PF00017; SHZ; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_bind; 1.
                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neopterygii, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontidae, Tetraodontidae, Tetraodon.
                                                                                                                                                         IVELFRNIAMKSAFVVERQPCAPAHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 764;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307106; AAL09415.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87411 MW; E661FFE18BEFD8BE CRC64;
                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , DB 2;
1.8e-54;
                                                                                                                                                                                                                                           764 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Mismatches
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.1%; Score 986;
83.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                             Tetraodon fluviatilis (Puffer fish)
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 191; Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00252; SH2
PROSITE; PS50001; SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              764 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=47145;
                                                                                                                                                           180
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Matches
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60 NGNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRP 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 QIACIGGPPKICLDRLETWITSLGEIQLQIRQQIKKLEELQQKVSYKGDPIIQHRPALEE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NHPTAAVVTEKQQMLEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; PS3_like_DNA_bnd.
InterPro; IPR001717; STAT.
                                                                                                                                                                RIVELFRNIAMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ol-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Signal transducer and activator of transcription (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                                                                                                                                                                                                                                                                                       Johnson M.C., Mourich D.V., Leong J.C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U60333; AAB60926.1; -.
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arredondo J.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT bint; 1.
SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;
                                                                                                                       Name=rbtStat3;
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%; Score 976; DB 2.
81.0%; Pred. No. 8e-54;
iive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163
767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque).
                                       01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 81.0%;
Matches 187; Conservative 2
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9544;
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DR EMBL; AF227560; AAF73401.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003654; C:nucleus; IEA.
DR GO; GO:0000365; P::egulation factor activity; IEA.
DR GO; GO:0007165; P::egulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P::egulation of transcription; IEA.
DR GO; GO:0007165; P::egulation of transcription; IEA.
DR GO; GO:0007165; P::egulation of transcription; IEA.
DR GO; GO:0007165; P::egulation of transcription of transcript
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Search completed: May 25, 2005, 17:43:44 Job time : 96.284 secs

sig Sta

Perfect score:

:10

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Mouse Sta
Human tru
                                                                                                            Human exp
Truncated
                                                                                                                                                                                                                                                                                                                                              The present sequence is mouse Stat3 mutant (V151A) protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained
                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Val substituted with Ala corresponds 151 position of Stat-3 protein" 213. .294 /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription, cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                            Human
                                                                                                                                     Human
                                                                                                                                                              Human
                          Mouse
                                                                                                                                             Human
                                                                                                                                                      Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
                                                                                                                                                                                                                                                                              Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids)
         Aay72860
Aay72851
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Aay72851
Aay72848
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Aay72819
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Abu04747 H
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                                        AAY72855
AAY72864
AAY72854
AAY72854
AAY72849
AAY72849
AAY72854
AAY72854
AAY72854
AAY72854
AAY72854
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AAY82957036
ABR59713
AAR72079
AAR72079
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                                                                                                                                                                                                                              AAY72863 standard; protein; 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00387418
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                  therapy; mutant; mutein.
Zhang X, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-226705/23.
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200116605-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                  Mus musculus
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11152
110090
110090
10040
10040
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6633
6633
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Region
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                                                                                                                                                                                                              RESULT 1
                                                                                                                                                                                                                       AAY72863
Mouse isc
Human Sta
Human pro
Mouse liv
Human STA
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Antipsori
Human PRO
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Rat Prote
Human pla
Human sig
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Murine ST
Human bai
                                                     May 25, 2005, 17:14:45; Search time 121.891 Seconds (without alignments) 726.619 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse
Human
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse
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                                                                                                       1 NHPTAAVVTEKQQMLEQHLQ.....IKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abg69497 H
Abul0476 N
Adn04365 A
Adp54789 H
Aab58442 I
Aab58442 I
Aab19964 H
Aab19964 H
Aae15174 H
                                                                                                                                                                                                                                                                                                                                                                                                                   Aay72850
Aay72846
Aay72841
Aay72861
Aay72862
Aae22055
Abb57164
Aae22056
Aae22056
Aae22056
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Aae22056
       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                 2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                           Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
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AAE22055
ABB57164
AAE22054
AAE22056
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AAB12377
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ABG69497
ABU10476
ADN04365
ADP54789
AAB58442
ADD44738
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AAB19964
AAE15174
                                                                                                                                 Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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geneseqp2000s:*
geneseqp2001s:*
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seq length: 200000000
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1172
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1168 1168 1168 1168 1157:10 1157:10 1157:1157 1157:1157 1157:1157 1157:1157 1157:1157

Score

Result 80.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to
by replacing Val 151 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c.Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, bNA binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.25
/note= "Stat3-c-Jun interaction region 1; corresponds
/note="Stat3" protein"
213. .229
                                                                                                                                                                                                                                                                                                                                                                                                    121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEBRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Stat3-c-Jun interaction region 2; corresponds 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                      1 NHPTAAVVTEKOOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                    NHPTAAVVTEKOOMLEOHLODARKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN
                                                                                                                                                                                                                                                                                                                   GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                              GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                           VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                          Length 229;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse Stat3 protein fragment #8 (130-358 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Darnell JE
                                                                                                                                                                                       ; Score 1172; DB 4;
; Pred. No. 6.5e-100;
0; Mismatches 0;
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                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-AUG-2000; 2000WO-US023822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00387418
                                                                                                                                                                                                         Best Local Similarity 100.
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-226705/23.
                                                                                                                                                             Sequence 229 AA;
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                                                                                                                                                                                                                                                                                                                       61
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                                     The present sequence is mouse Stat3 protein fragment containing 130-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                GINIQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDBELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                               1 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                          Score 1168; DB 4; Length 229; Pred. No. 1.5e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236. .252
/note= "Stat3-c-Jun interaction region 2;
342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse Stat3 protein fragment #4 (107-358 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Horvath C, Wrzeszcynska MH, Darnell JE;
                                                                                                                                                                                                                                                                                                              0; Mismatches
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               65; Page 76-77; 86pp; English.
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Best Local Similarity 99.6%;
Matches 228; Conservative
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                                                                                                                                                                                                                                               Sequence 229 AA;
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31-AUG-1999;
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24-SEP-1993;
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27-SEP-1995
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                                                                                          The present sequence is mouse Stat3 protein fragment containing 107-358 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, colled-coil domain, binding domain, linker domain, SH2 domain and transactivation domain
                                                                                                                                                                                                                                                                                                                                                83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                       24 NHPTAAVVTEKQOMLEQHLODVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMODLN
                                                                                                                                                                                                                                                                                                                                                                                        84 GNNQSVTRQKWQQLEQMLTALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                                                                                                                                                                                                                                                                                                                                        121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                       144 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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                                  Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                         Length 252;
                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                        Score 1168; DB 4;
Pred. No. 1.7e-99;
0; Mismatches 1;
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                                                                      Claim 65; Page 73; 86pp; English
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Best Local Similarity 99.6%;
Matches 228; Conservative
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                                                                                                                                                                                                                                               Sequence 252 AA;
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61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal transducer and activator of transcription; STAT; 19sf6; Stat3; receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is mouse Stat3 protein fragment containing 107-377 amino acids of Stat3 protein. This Stat3 fragment showed strong binding to c-Jun protein in the cell extract. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of typroliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                                                                       Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.7%; Score 1168; DB 4; Length 271; 99.6%; Pred. No. 1.9e-99; ive 0; Mismatches 1; Indels
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                                                                                                                                                       Darnell JE;
                                                                                                                                                       Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 65; Page 67-68; 86pp; English
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99US-00387418.
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93US-00126595.
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Matches 228; Conservative
                                                                           (UYRQ ) UNIV ROCKEFELLER
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                                                                                                                                                       Zhang X, Horvath C,
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                                                                                                                                                                                                                               WPI; 20'01-226705/23.
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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/note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
                                                                                                                                                                                                                   New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g. oncogenesis, inflammation, parasitic disease or autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse, Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                Mouse signal transducer and activator of transcription (STAT) protein STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery vi DNA binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNNQSVTRQKMQQLEQMLTALDQMRRSIVSBLAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GINGSVIRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKILIDDEELADWKRRPBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.7%; Score 1168; DB 2;
99.6%; Pred. No. 7.5e-99;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                  Disclosure; Page 87-90; 138pp; English.
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                                                                                                                           Horvath CM,
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               95WO-US017025
                                                     95US-00369796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activation of transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.6
Matches 228; Conservative
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                                                                                       (UYRQ ) UNIV ROCKEFELLER
                                                                                                                               Wen Z,
                                                                                                                                                                   WPI; 1996-333941/33.
                                                                                                                                                                                       N-PSDB; AAT31280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 770 AA;
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                                                                                                                             Darnell JE,
               28-DEC-1995;
                                                     06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                              A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAQ89338) was isolated that encoded a 91 KDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAQ89339-40) were cloned in plasmids 138fl and 198f6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKWKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 GNNÇSVIRÇEMÜÇLEÇMLTALDÇMRRSIVSELAGLLSAMEYVÇKTLTDEELADWKRRPBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAT, STAT4; signal transducer and activator of transcription; DNA binding protein; ligand; receptor; oncogenesis; inflammation; autoimmune disease; antagonist; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.7%; Score 1168; DB 2; Length 770; 99.6%; Pred. No. 7.5e-99; ive 0; Mismatches 1; Indels (
                                                                                               2
                                                                                               Zhong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398. .508
/label= DNA_binding_domain
/note= "Claim 3, page 110"
                                                                                                 Wen
                                                                                                                                                                                                                                                                    Claim 1; Page 107-110; 160pp; English.
                                                                                                 Shuai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW03176 standard; protein; 770 AA
   94US-00212184.
94US-00212185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                 Schindler CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                           UYRQ ) UNIV ROCKEFELLER
                                                                                                                                       WPI; 1995-139598/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 228; Conserv
                                                                                                                                                           N-PSDB; AAQ89340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9620954-A2
   11-MAR-1994;
11-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse STAT4
                                                                                               Darnell JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW03176;
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Key Domain Mus sp.

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(UYRQ ) UNIV ROCKEFELLER
    therapy; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-226705/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 228 AA;
                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                    WO200116605-A2
                                                                                                                                                                                                                                                                                                                         31-AUG-1999;
                            Mus musculus
                                                                                                                                                                                                                                                                            08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                        Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                              Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                    containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing Leu 148 with Ala in Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, colled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
            'note= "Wild type Leu substituted with Ala; corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription; cellular transformation; dysproliferative disease; cancer; psoriasis;
                       to 148 position of Stat-3 protein"
213. 229
Motes "Stat1-c-Jun interaction region 2; corresponds 342-358 position of Stat3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NHPTAAVVTEKOOMLEQHLODARKRVODLEQKWKVVENLODDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                            present sequence is mouse Stat3 mutant (L148A) protein fraqment
                                                                                                                                                                                                                                                Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.2%; Score 1163; DB 4; Length 229; Best Local Similarity 99.1%; Pred. No. 4.4e-99; Matches 227; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse Stat3 mutant (T346A, K348A, R350A) protein fragment.
                                                                                                                                                                                                   Darnell JE;
                                                                                                                                                                                                   Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Æ
                                                                                                                                                                                                                                                                                    Claim 66; Page 85; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY72861 standard; protein; 228
                                                                                                                              30-AUG-2000; 2000WO-US023822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                          (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                  Zhang X, Horvath C,
                                                                                                                                                                                                                        WPI; 2001-226705/23
Misc-difference 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 229 AA;
                                                                                WO200116605-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-2001
                                                                                                        08-MAR-2001
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                                   Region
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The present sequence is mouse Stat3 mutant protein fragment containing 130-358 amino acids of Stat3 protein. This mutant is obtained by replacing Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as C-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These indentifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain, linker domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 179
                                                               /note= "Stat3-c-Jun interaction region 1; corresponds to 110-154 position of Stat3 protein"
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                                                                                                                                                                                                                                          /note= "Wild type Thr substituted with Ala; corresponds to 346 position of Stat-3 protein" Misc-difference 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild type Arg substituted with Ala; corresponds to 350 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                           substituted with Ala; corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NHPTAAVVTEKQQMLEQHLQD-RKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying an agent for use in modulating the interaction between transcription factor c-Jun and a Stat3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Length 228;
                                                                                                "...s.cu. 213. .229 ------ of stat3 protein" /note= "Stat3-c-Jun interaction region 2; 342-358 position of Stat3 protein" Misc-difference 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1157.5; DB 4; Length
Pred. No. 1.4e-98;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild type Lys substituted v
to 348 position of Stat-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wrzeszcynska MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 66; Page 84-85; 86pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00387418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-AUG-2000; 2000WO-US023822
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Best Local Similarity 99.6
Matches 228; Conservative
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Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypostais stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis, adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis, sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; drave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion; Statbeta.
180 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               713. .714
/note= "Encoded by ACA CCA TTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dalton W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 713. .714
                                                                                                                                                                                AAE22055 standard; protein; 720 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-2001; 2001WO-US028254.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYJO ) UNIV JOHNS HOPKINS. (UYSF-) UNIV SOUTH FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pardoll D, Jove R,
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Human Stat3beta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-362218/39.
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                                                                                                                                                                                                                                                     AAE22055;
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular 98.7%; Score 1157; DB 5; 98.7%; Pred. No. 7.2e-98; Nagata T, (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON 1; Mismatches Claim 2; Page 1084-1087; 2690pp; English. Takahashi Y, ABB57164 standard; protein; 769 AA. 18-MAY-2001; 2001WO-JP004192. 18-MAY-2000; 2000JP-00145977. (first entry) Query Match
Best Local Similarity 98.73
Matches 226; Conservative Asai S, WPI; 2002-034733/04. N-PSDB; ABI99454. Stat3beta protein Sequence 720 AA; WO200188188-A2 Mus musculus 07-MAR-2002 Ishikawa K, 22-NOV-2001. ABB57164; 250 181 310 genes. ABB57164 RESULT 8888888888888 g 엄 유 ઠે 셤 8 ð ð The invention relates to a method of modulating angiogeneeis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogeneeis is useful for treating or preventing hypoxic or ischaemia, condition or disorder which is the result of stroke, ischaemia, coronary atheroscalerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, pypoglycaemia, chicrogen necrosis, poliferative angiopathy e.g. diabetic microangiopathy nitrogen necrosis, poliferative angiopathy e.g. diabetic microangiopathy with necvascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autonimmune disease such as systemic lupus erychematosus, multiple sclerosis, insulin dependent diabetes mellitus, sjoren's syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, permicious anaemia, autodimmune thyroidtis, autoimmune thyroidtis, autoimmune thyroidtis, autoimmune neutropenia, myasthenia gravis, Disclosure; Page 87-89; 94pp; English.

ö ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309 Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating especific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human 121 ACIGGPPNICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 1 NHPTAAVVTEKOOMLEOHLODARKRVODLEOKMKVVENLODDFDFNYKTLKSQGDMQDLN Mouse ischaemic condition related protein sequence SEQ ID NO:398. .; 0 VELFRNIAKSAFVVEROPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229 Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease. Length 720; Ishii Y;

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genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequence in ABB57020 to ABB57347) or by determining the expression profile of a gene group comprising these genes. The expression lidicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                Length 769;
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Pred. No. 7.8e-98;
1; Mismatches 2;
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98.7%;
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The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription of 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, inflammation, tissue ischaemia or postructive pulmonary disease, choking, asphyxia, hypoglycaemia, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, chitogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliotating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, sjopren's syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious canaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, contentive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, vitiligo, contentity, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating contentions of plantary archinoms of proprietions.
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                                                                                          Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is also used in gene therapy. The present sequence is human Stat3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The
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                                                                                                                                                                                                             Disclosure; Page 83-85; 94pp; English.
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                                              N-PSDB; AAD35065
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Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stazis, coronary atherosclarosis; wascular occlusion; hypoxia; stroke, anglogenesis myocardial inferction; hypoglycaemia; inflammation chronic obstructive pulmonary disease; cardiac arrest; inflammation chronic obstructive pulmonary disease; cardiac arrest; inflammation chronic active hepatitis; adult respiratory disease; pepilepsy; slocks; chronic active hepatitis; adult respiratory disease; pepilepsy; polywysticis; theumaticid arthritis; autoimmune infertility; aneamia; proliferative disease; farave's disease; ulcerative colitis; arcoma; carcinoma; degenerative disease; praced arthritis; autoimmune infertility; aneamia; proliferative disease; farave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative diseorder; gene therapy; growth deficiency; carcinoma; degenerative diseorder; peocyter; lesion.

Homo sapiens.

WO200220032-Al.

14-MAR-2002.

10-SEP-2001; 2001WO-U8028254.

08-SEP-2000; 2000WS-0231212P.

(UWJC) PHULY GONTH FLORIDA.

WHI; 2002-362218/39.

Wodulating angiogenesis and an immune response in an individual, for treating any progenesis and an immune response in the modulates the activity of a signal transducer and activator compound that modulates the activity of a signal transducer and activator of transcription 3.

Disclosure, Page 83-85; 94pp; English.

The invention relates to a method of modulating angiogenesis and immune response. Wendon involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Sta23). Modulating angiogenesis is useful for treating or preventing hypoxic or ischemia or postnatal oxygen deprivation, suffocation, inflammation 3 (Sta23). Modulating angiogenesis is useful for treating or preventing hypoxic or ischemia and the lower extrematices, infarcing the result or transcription 3 (Sta23). Modulating angiogenesis is useful for treating or preventing hypoxic or ischemia or oronary atherosclerosis, myocardial i

The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atheroselerosis, myocardial infarction, inflammation, tischaemia, coronary atheroselerosis, myocardial infarction, inflammation, tischaemia, prenatal or postnatal oxygen deprivation, suffocation, shock coronary augmentary disease, choking, asphyxia, hypoglycaemia, collusion, prenatal or postnatal oxygen deprivation, suffocation, shock coronary apulmonary disease, choking, asphyxia, hypoglycaemia, colluspsy, emphysema, adult respiratory distress syndrome, cardiac arrest, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus crythematosus, multiple sclerosis, insulin dependent diabetes mellitus, sjogram, scleroderma, polymyositis, chronic active hepatitis, carded connective tissue disease, primary bilary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia puppura, Grave's disease, colopatics, autoimmune thyroiditis, cirrhosis, pemphigus vulgaris, autoimmune coliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, colon sarcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, chrones e generalive disorders, physical tramma, lengenence is human ccopenia regulation related to angiogenesis regulation

Sequence 769 AA;

Query Match
98.7%; Score 1157; DB 5; Length 769;
Best Local Similarity 98.7%; Pred. No. 7.8e-98;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 60

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ö ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180 250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309 The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. ARFF-inhibitors, e.g. antibodies, antisense oligonuclectides or ribozymes, may be used to treat diseases induced by IL-6, e.g. 130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQXKVVENLQDDFDFNYKTLKSQGDMQDLN 189 Mouse, acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy. New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI 1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN ; 0 Length 770; VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 2; Indels 98.7%; Score 1157; DB 2; 98.7%; Pred. No. 7.8e-98; iive 1; Mismatches 2 Mouse liver acute phase response factor. Claim 10; Page 20-22; 31pp; English. AAR82995 standard; protein; 770 AA. 95EP-00104670. (first entry) 226; Conservative Akira S, Kishimoto T; WPI; 1995-346089/45. N-PSDB; AAT05619. (KISH/) KISHIMOTO T. Query Match Best Local Similarity hypertension, etc Sequence 770 AA; 29-MAR-1995; 04-APR-1994; 25-MAR-1996 Mus musculus 11-0CT-1995. EP676469-A2. AAR82995; 310 190 121 181 61 diseases RESULT 13 à g à 셤 ð d à

309

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The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-
    121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.
                    250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                         signal transducer and activator of transcription; crystal;
                                                                     310 VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                       VELPRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                             19. .21
/label= 3(10) helix of alpha helix 2
28. .33
/label= Alpha helix 3
35. .40
/label= Alpha helix 4
43. .47
/label= Alpha helix 5
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                                                                                                                                                                                                                                N-terminal domain of murine STAT-3 protein.
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/label= Alpha helix 2
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                                                                                                                                                  AAB12377 standard; peptide; 770
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                                                                                                                                                                                                                                                                       drug design; murine
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                                                                                                                                                                                                                                                                                                            Signal Transducer and Activator of Transcription 3; STAT3; allele; II-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
                                                     ACIGGPPNI CLDRIENWI TSLAESQLOTRQOIKKIBELQQKVSYKGDPIVQHRPMLEBRI
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                                                                                                                      Score 1157; DB 2; Length 770;
Pred. No. 7.8e-98;
1; Mismatches 2; Indels
                                                                                                        VELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLVKFPEL
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                                                                                                                                                                                                    AAY03768 standard; protein; 770 AA.
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                                                                                                                                                                                                                                                                                   Human STAT3 allelic variant.
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Best Local Similarity 98.7
Matches 226; Conservative
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N-PSDB; AAX29281.
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98.7%; Score 1157; DB 3; Length 770;
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Matches 226; Conservative 1; Mismatches 2; Indels (
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Sequence 18, Application US/09387418A
Patent No. 6391572
GENERAL INPORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-82-09-12

US-08-96-65-12

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US-08-948-547-12

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US-09-387-418A-31

Sequence 31, Application US/09387418A

Patent No. 6391572

GENERAL INFORMATION:
APPLICANT: With Mareseczynska, Melissa H
APPLICANT: Darnell Jr. James E

APPLICANT: Darnell Jr. James E

APPLICANT: Darnell Jr. James E

APPLICANT: NETROROS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253

CURRENT APPLICATION UNMERS: US/09/387,418A

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43
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US-08-781-890-14
US-09-387-418A-19
US-09-387-418A-19
US-09-387-418A-12
US-09-387-418A-22
US-09-387-418A-23
US-09-387-418A-21
US-09-387-418A-21
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US-09-387-418A-17
                                                                                                                                                                                                                                                                     ALIGNMENTS
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  ORGANISM: Mus musculus
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IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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                                                181 VELFRNLAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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                      FKVRLLVKFPEL 229
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Pred. No. 7.1e-99;
0; Mismatches 1;
                      181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT
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Sequence 9, Application US/09387418A;
Fatent No. 631572
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Wrzeszczynaka, Melissa H
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
TITLE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 9
LENGTH: 271
LENGTH: 271
                                                                                                                                                                  Sequence 14, Application US/09387418A

Patent NO. 6391572

GENERAL INFORMATION:
APPLICANT: Chang, Xiaokui
APPLICANT: Wrzesczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 99.6%;
Matches 228; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Mus musculus
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ORGANISM: Mus musculus
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Best Local Similarity
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                                                                                                                                RESULT 4
US-09-387-418A-14
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LENGTH: 252
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Patent No. 6391572
GENERAL INFORMATION:
APPLICANT: ADARD, VISIAGE, Melissa H
APPLICANT: Barnell Jr., James E
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQIENCE: 400-1-253
NUMBER OF SEQIENCE: 400-1-253
NUMBER OF SEQIENCE: 400-1-253
                APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REPERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
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Pred. No. 6.3e-99;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                              Length 229;
                                                                                                                                                                                                                                                                                                                            Score 1168; DB 3;
Pred. No. 6.3e-99;
0; Mismatches 1;
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99.6%;
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Best Local Similarity 99.6%;
Matches 228; Conservative C
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Horvath, Curt M
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Matches 228; Conservative
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US-09-387-418A-18
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LENGTH: 22
APPLICANT:
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Sequence 12, Application US/08852091
Patent No. 5883228
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zilong Yen
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
                                                                             250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
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                                                 121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
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SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAMME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSE: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 60.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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: USA
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US-08-852-091-12
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Patent No. 5716622
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Zhong Zhong
TITLE OP INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OP INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
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                                                                                                                                              61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                           84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
                                                                                                                                                                                                                                                 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                             130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                  83
                                                                             24 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                              1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Mismatches
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FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY AGENT INPORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELEPHONE: 201 447-5800
TELEPHONE: 201 343-1684
TELEX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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amino acid
Conservative
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| Sequence 12, Application US/08820754 |
| Patent No. 5976835 |
| GENERAL INCRMATION: Schindler, Christian W. PAPLICAWT: Schindler, Christian W. APPLICAWT: Schindler, Christian W. APPLICAWT: Schindler, Christian W. APPLICAWT: Wen, Zilong APPLICAWT: APPLICAWT: Wen, Zilong INTILE OF INWENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INWENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES AND METHODS OF USE THEREOF STATE: 411 Hackensack Avenue CITY: Hackensack Avenue CITY: Hackensack Avenue CITY: Hackensack Compatible 
                        181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                      310 VELFRNLMKSAFVVERQPCMPWHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
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Pred. No. 3e-98;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600-1-073 CIP
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
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Best Local Similarity 99.6%;
Matches 228; Conservative C
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                                                                                                                                                                                                                                  US-08-820-754-12
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190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                             121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                  250 ACIGGPPNICLDRLENWITSLABSQLQTRQQIKKLBELQQKVSYKGDPIVQHRPMLEBRI 309
                                                                                                                                                                                                                                                           310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                             VELFRNIAKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26,742
ep. 600-1-073 CIP
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CLASSIFICATION:
PRIOR PAPELICATION:
PRIOR PAPELICATION DATA:
PRIOR PAPELICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-MOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
PRIOR APPLICATION UNBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY AGENT: 14-SEP-1993
FILING DATE: 24-SEP-1993
FILING DATE: 24-SEP-1993
ATTORNEY AGENT: US 08/126,588
FILING DATE: 24-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                   US-08-956-652-12; Sequence 12, Application US/08956652; Patent No. 6013475; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-956-652-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
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TELECOMMUNICATION INFORMATION:
                                                                                  Query Match
Best Local Similarity 99.67
Matches 228; Conservative
                          ) MOLECULE TYPE: protein US-08-956-869-12
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 07601
        TOPOLOGY:
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STATE:
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                                                                                    61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                              121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                          1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLN 60
                          Gaps
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                                                                                                                                                                                                                                                                                            181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF OWNERS OF SEQUENCES: 25 CORRESPONDENCE ADDRESS:
                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
    Pred. No. 3e-98;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEE-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08956869
Fatent No. 6030808
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E. APPLICANT: Schindler, Christian W. APPLICANT: Wr., Xian-tuan APPLICANT: Wen, Zilong APPLICANT: Zhong, Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/956,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,185
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
Best Local Similarity 99.6%;
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 770 amino acids
amino acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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US-08-956-869-12
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61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLN 60
                                                                                                                                                                                                                                                                                       190 GNNQSVTRQKWQQLEQMLTALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
                                                                    Gaps
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| Patent No. 6124118
| GENERAL INFORMATION:
| APPLICANT: Dariell Jr., James E.
| APPLICANT: Bariell Jr., James E.
| TITLE OF INVENTION: RECEPTOR RECCGNITION FACTORS, PROTEIN TITLE OF INVENTION: BEQUENCES: 25
| CORRESPONDENCE ADDRESS: ADDRESSE: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack Avenue CITY: Hackensack Avenue
Score 1168; DB 3; Length 770;
Pred. No. 3e-98;
0; Mismatches 1; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
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ER: 600-1-073 CIP
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 2-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
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      99.7%;
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FILING DATE
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STREET: 41
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                                                                                                                                                                                                                           SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REPERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT APPLICATION DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                1 NHPTAAVVTEKOOMLEQHLODARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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3e-98;
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Pred. No. 3e-98;
0; Mismatches
                                                                                                                                                                                 Score 1168; D
Pred. No. 3e-9
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09364970
Patent No. 6235873
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acids
                                                                                                                                                                                 99.7%;
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                                                                                                                                                                               Query Match
Best Local Similarity 99.6
Matches 228; Conservative
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Matches 228; Conservative
                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12
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US-09-364-970-3
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US-09-364-970-5

Sequence 5, Application US/09364970

Sequence 5, Application US/09364970

Sequence 5, Application US/09364970

Sequence 5, Application USS Sequence

APPLICANT: Browberg, Jacqueline

TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR

TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING

TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES

FILE REFERENCE: 600-1-252

CURRENT APPLICATION NUMBER: US/09/364,970

CURRENT FILING DATE: 199-07-31

NUMBER OF SEQ ID NOS: 10

SOCTIVER: PATENTIN Ver. 2.0
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Sequence 12.

Patent No. 6338949

GENERAL INFORMATION:

APPLICANT: Darnell Jr., James E.

APPLICANT: Schindler, Christian W.

APPLICANT: Fu, Xian-Yuan

APPLICANT: Zhong

APPLICANT: Zhong

APPLICANT: Zhong

TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.7%; Score 1168; DB 3;
99.6%; Pred. No. 3e-98;
iive 0; Mismatches 1;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
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411 Hackensack Avenue
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Best Local Similarity 99.6
Matches 228; Conservative
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ORGANISM: Mus musculus
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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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Patent No. 6605442
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Pu, Xian-Yuan
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                            APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SRE-1993
ATTORNEY, AGENT INFORMATION:
JMBER: US 07/980,498
23-NOV-1992
                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMINICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX. 13351
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 770 amino acids amino acids
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Matches 228; Conservative
                        FILING DATE: 23-NOV-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
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  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-956-653A-12
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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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Pred. No. 3e-98;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                  PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-8EP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: May 25, 2005, 17:47:41
Job time : 29.6534 secs
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.6%;
Matches 228; Conservative
                                        11-MAR-1994
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amino acid
CURRENT APPLICATION DATA:
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LENGTH: 770 amino aci
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                                               FILING DATE: 11
CLASSIFICATION:
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May 25, 2005, 17:36:58 ; Search time 100.287 Seconds (without alignments) 763.830 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	0-01	0-01	0-01	0-01	0-01	9-60	9-01	0-01	10-3	10-3	10-3	0-01	0-01
ID	ns-	ns-	us-	ns-	ns-	US-09-876-773-12	ns-	ns-	ns-	ns-	ns-	us-	ns-
DB	13	13	13	13	13	11	17	13	15	15	15	14	14
* Query Match Length DB	229	229	229	252	271	770	770	229	720	769	769	770	170
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Sequence 2, Appli Sequence 780, App Sequence 329, App Sequence 329, App Sequence 29, Appl Sequence 19, Appl Sequence 19, Appl Sequence 22, Appl Sequence 22, Appl Sequence 24, Appli Sequence 35, Appli Sequence 35, Appli Sequence 352, Appli Sequence 352, Appli Sequence 352, Appli Sequence 823, Appli	Sequence 6, Appli Sequence 8, Appli
14 US-10-117-087-2 9 US-09-925-302-780 15 US-10-116-275-329 15 US-10-116-275-329 13 US-10-116-275-349 13 US-10-090-185-29 13 US-10-090-185-19 13 US-10-090-185-13 13 US-10-090-185-21 13 US-10-090-185-21 13 US-10-090-185-21 13 US-10-090-185-21 14 US-10-090-185-21 15 US-10-090-185-21 16 US-10-090-185-21 17 US-10-090-185-21 18 US-10-090-185-21 19 US-09-876-773-6 11 US-10-876-773-6 11 US-10-876-773-4 14 US-10-876-773-4 14 US-10-876-773-4 14 US-10-876-773-4 15 US-10-876-773-4 16 US-10-876-773-4 17 US-10-876-773-4 18 US-10-876-773-4 19 US-10-876-773-4 10 US-10-876-773-4 11 US-10-876-773-4 12 US-10-876-773-4 13 US-10-876-773-4 14 US-10-876-773-4 17 US-10-876-773-4 17 US-10-876-773-4 18 US-10-876-773-4 19 US-10-876-773-4 10 US-10-876-773-4 17 US-10-876-775-889-823 17 US-10-89-823-17-80	9 US-09-833-205-6 11 US-09-876-773-8
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7.2111 1.2211 1.22111	562 562
4 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 5

## ALIGNMENTS

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Sequence 31, Application US/10090185

Publication No. US20020197647A1

GENERAL INFORMATION:

APPLICANT: Wizeszynska, Melissa H

TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-1-253

CURRENT APPLICATION NUMBER: 2002-03-04

FRIGN APPLICATION NUMBER: 09/387,418

PRIOR APPLICATION NUMBER: 09/387,418

WINDER OF OTH WAS 05-01 NUMBER: 05-01 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 229; Conservative
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ORGANISM: Mus musculus
US-10-090-185-31
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LENGTH: 229
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IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
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Pred. No. 1.9e-94;
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Pred. No. 1.7e-94;
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; Fublication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wireszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Horvath, Curt M
; APPLICANT: Horvath, Curt M
; TITLE OF INVENTION: INTERACTIONS; FILE REPRENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT PELLING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PATENTIN VET. 2.0
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Best Local Similarity 99.6%;
Matches 228; Conservative (
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LENGTH: 229
TYPE: PRT
ORGANISM: Mus musculus
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Publication No. US20020197647A1

GENERAL INFORMATION

APPLICANT: Zhang, Xiaokui

APPLICANT: Wrzeszczynska, Melissa H

APPLICANT: Horveth, Cutr M

APPLICANT: HORVETHON: INFERACTIONS

TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR F

TITLE OF INVENTION: MYERACTIONS

FILE REFERENCE: 600-1-253

CURRENT APPLICATION NUMBER: US/10/090,185

CURRENT APPLICATION NUMBER: 09/387,418

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN Ver: 2.0
                                                                                                                                                                                                                                                                                                            APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: INTERACTIONS
FILE OF INVENTION: INTERACTIONS
FILE OF INVENTION: INTERACTIONS
FILE OF INVENTION: NUMBER: US/10/090,185
CURRENT APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
NUMBER: OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
                                 121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ACIGGPPNICLDRLENWITSLAESQLQTRQDIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
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Pred. No. 1.7e-94;
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                                                                                                                                                                                                                                              Sequence 18, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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120

RESULT 5 US-10-090-185-9

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130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLM 189
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                       FILING DATE: 11-MAR-1994

APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992

APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992

APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993

APPLICATION NUMBER: WO 08/126,588
FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: JACKSON ESQ., David A.

REGISTRAATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.7%; Score 1168; DB 11
99.6%; Pred. No. 7.9e-94;
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Publication No. US20050079543A1
GENERAL INFORMATION:
Schindler, Christian W.
FW. Xian-Yuan
Wen, Zilong
Zhong, Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 770 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Klauber
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STATE: New Jersey
COUNTRY: USA
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Matches 228; Conservative
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US-10-639-617-12
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                                                                                         APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Barnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR I
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT FILING DATE: 2002-03-04
FRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLLN
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TITLE OF INVENTION: RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 271;
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
PRIOR APPLICATION: A35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1168; DB 13
Pred. No. 2.1e-94;
0; Mismatches 1
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ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian
Fu, Xian-Yuan
Wen, Zilong
Sequence 9, Application US/10090185
Publication No. US20020197647A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.6%;
Matches 228; Conservative
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COMPUTER READABLE FORM:
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STATE: New Jersey
                                                                          APPLICANT: Zhang, Xiaokui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus US-10-090-185-9
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                                                   GENERAL INFORMATION:
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LENGTH: 271
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APPLICANT: Yu, Hua
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Jove, Richard
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
TITLE OF INVENTION: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 6/231,212
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                            1 NHPTAAVVTEKQQMEEQHAQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 60
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                                                                                                                                                                                                                                                                                                            61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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                                                                                                        Length 229;
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Pred. No. 6.7e-93;
1; Mismatches 2; Indels 0
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                                                                                                                                                      Indels
                                                                                                   Score 1163; DB 13;
Pred. No. 4.6e-94;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/10380020
; Publication No. US20040052762A1
                                                                                                      99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 720
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Best Local Similarity 98.7%;
Matches 226; Conservative
                                                                                                                                                         Conservative
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                          musculus
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ORGANISM: Homo Sapiens
                                                                                                   Query Match
Best Local Similarity
Matches 227; Conserv
TYPE: PRT
ORGANISM: Mus
                             ; ORGANISM. US-10-090-185-30
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US-10-380-020-2
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| Sequence 30. Application US/10090185
| Publication No. US20020197647A1
| Publication No. US20020197647A1
| GENERAL INFORMATION:
| APPLICANT: Zhang, Xiaokui
| APPLICANT: Wrzeszczynska, Melissa H
| APPLICANT: Darnell Jr., James E
| TITLE OF INVENTION: MPRER: US/10/090,185
| CURRENT APPLICATION NUMBER: US/10/090,185
| CURRENT PILING DATE: 2002-03-04
| PRIOR FILING DATE: 1999-08-31
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE: Patentin Ver: 2.0
| LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
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                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.7%; Score 1168; DB 17
Best Local Similarity 99.6%; Pred. No. 7.9e-94;
Matches 228; Conservative 0; Mismatches 1
                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY AGENT INFORMATION:
                APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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SEQUENCE CHARACTERISTICS:
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121 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                                                                           250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
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Darnell, Jr., James E.
Kuriyan, John
TITLE OF INVENTION: A CYNSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
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Pred. No. 7.3e-93;
1; Mismatches 2; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION & Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/09/012,710
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: JACKEON ESQ., DAVIG A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackbon
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                             ; Sequence 8, Application US/10045792; Publication No. US20030003563A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Vinkemeier, Uwe
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Best Local Similarity 98.7%;
Matches 226; Conservative
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COMPUTER READABLE FORM:
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COUNTRY: USA
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                                                                                                                                                                                                                                                     RESULT 12
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                     APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Dave, Richard
APPLICANT: Jove, Richard
APPLICANT: John, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
TITLE REPERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: 60/231,212
PRIOR PAPLICATION NUMBER: 60/231,212
PRIOR PLICATION DATE: 2000-99-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pardoll, Drew
APPLICANT: Dalton, Willian
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.7%; Score 1157; DB 15; Best Local Similarity 98.7%; Pred. No. 7.3e-93; Matches 226; Conservative 1; Mismatches 2;
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Pred. No. 7.3e-93;
1; Mismatches 2;
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.7
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo Sapiens
US-10-380-020-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo Sapiens
  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                       169
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US-10-380-020-5
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                                                                                                                                                                                                                                                                                                                                               TYPE: PRT<
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ORGANISM: Human
        US-10-117-087-2
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ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 180
                      250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI 309
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                                                                                                                                                                    RESULT 13
US-10-038-010-56

sequence 56, Application US/10038010
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFRENCE: 8476A7
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT APPLICATION NUMBER: US 60/259,377
PRIOR APPLICATION NUMBER: US 60/259,377
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 56
LENGTH: 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNNOSVTROKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRRPEI
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Publication No. US20030166854A1
GENERAL INFORMATION:
APPLICANT: SERLUPI-CRESCENZI, Ottaviano
FILE SERLORICES SERLUPI-Z
CURRENT APPLICATION ALLELIC VARIANTS OF HUMAN STAT3
FILE REFERENCE: SERLUPI-2
CURRENT PILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US/10/117,087
CURRENT FILING DATE: 2000-03-19
PRIOR FILING DATE: 2000-03-19
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: STAT3 : Transcription factor is LOCATION: (1)..(770)
US-10-038-010-56
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Best Local Similarity 98.7%;
Matches 226; Conservative
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SEQ ID NO 2
LENGTH: 770
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US-10-117-087-2
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                                                                                                                                                              130 NHPTAAVVTEKOOMLEOHLODVRKRVODLEOKMKVVENLODDFDFNYKTLKSOGDMODLN 189
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                                                                                                           1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                       61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI
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Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 780, Application US/09925302
| Sequence 780, Application US/09925302
| Patent No. US20020044941A1
| GENERAL INPORMATION:
| APPLICANT: Rosen et al. |
| TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies |
| FILE REFERENCE: PA104
| CURRENT APPLICATION NUMBER: US/09/925,302
| CURRENT FILING DATE: 2001-08-10
| PRIOR PELING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 8966
| SOFTWARE: Patentin Ver. 2.0
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                                                        Indels
  Score 1157; DB 14
Pred. No. 7.3e-93;
                                                        1; Mismatches
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  98.7%;
98.7%;
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Best Local Similarity 98.73
Matches 226; Conservative
                                                        Matches 226; Conservative
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ORGANISM: Homo sapiens
  Query Match
Best Local Similarity
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US-09-925-302-780
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Genčore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                    Copyright
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OM protein - protein search, using sw model

Run on:

25, 2005, 17:24:07; Search time 21.6038 Seconds (without alignments) 1019.898 Million cell updates/sec

US-10-090-185-31 1172 Title: Perfect score:

1 NHPTAAVVTEKQQMLEQHLQ.....IKTGVQFTTKVRLLVKFPEL 229 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ISGF3 p91-related	DNA-binding protei	interferon-depende	gamma-interferon a	interferon alpha-i	mammary gland fact		transcription acti	mammary gland fact	interleukin-4-indu	DNA-Binding Protei	chromosome segrega	hypothetical prote	conserved hypothet	hypothetical prote	myosin heavy chain	tpr protein - huma	ote	median body protei	myosin heavy chain	myosin heavy chain	microtubule bindin	myosin heavy chain	nuclear/mitotic ap	epimorphin - mouse	myosin heavy chain	tropomyosin 2, ske	hypothetical prote	hypothetical prote
SUMMARIES	ID	149508	A54444	A46159	A56047	A46160	149274	S54772	G02317	S55527	A54740	157557	AE1947	G72593	A70387	T27075	A27224	S33124	C64527	S33821	806117	S21801	T13030	B43402	T30336	S51193	A59252	S24401	20	T51505
	DB	7	7	0	~	7	7	0	~	~	7	~	~	~	~	7	-	~	7	~	~	-	~	-	~	~	~	~	~	7
	Length	770	770	739	748	851	786	793	794	794	848	837	1208	533	978	1166	1509	2094	284	857	924	1999	1690	2007	2253	289	1976	æ	734	853
مد	Query	98.7	98.3	44.7	m	27.5	22.9	22.9	2	20.5	10.8	10.7	10.5	10.4	10.4	10.3	6.6		9.8		9.7		9.6		9.6	9.6			9.5	
	Score	1157	1152	523.5	508	322	268.5	268.5	262.5	237	127	125.5	122.5	122	122	120.5	116.5	116.5	114.5	114.5	113.5	113	112.5	112.5	112.5	112	112	111	111	111
	Result No.	-	7	3	4	co.	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

A54444 DNA-binding protein APRF - human

RESULT 2

hypothetical prote	chromosome segrega	interaptin - slime	hypothetical prote	microtubule bindin	hypothetical prote	exonuclease (EC 3.	hypothetical coile	centrosome associa	myosin heavy chain	364K Golgi complex	SCP1 protein - rat	myosin heavy chain	myosin heavy chain	desmoplakin I - hu	myosin heavy chain
T24806	G83960	T14867	T43448	H90279	AC1814	BVECSC	T38077	T08621	A33977	JC5837	S28061	A59287	A47297	A38194	833068
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1164	1188	1738	434	464	727	1048	1957	2442	1959	3187	946	1940	1992	2677	527
9.5	9.5	9.4	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.5	9.5
111	111	110.5	109.5	109.5	109.5	109.5	109.5	109.5	109	109	108.5	108.5	108.5	108	107.5
. 6	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45

## ALIGNMENTS

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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 149508; 149009
R; AkIra, S.; Mishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sur A; Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr A; Reference number: A54444; MUID:94208062; PMID:7512451
A; Accession: 149508
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-770 cRES
A; Residues: 1-770 cRES
A; Residues: 1-770 cRES
A; Residues: 1-770 cRES
A; Cross-references: UNIPROT:P42227; GB:L29278; NID:9476715; PIDN:AAA37254.1; PID:947671
B; R; Baz, R.; Durbin, J.B.; Levy, D.B.
J; Biol. Chem. 269, 24391-24395, 1994
A; Title: Acute phase response factor and additional members of the interferon-stimulates A; Accession: 149009
A; Accession: 149009
A; Accession: 149009
A; Accession: 149009
A; Accession: Labour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-393,'M',395-700,702-770 <RE2>
A;Cross-references: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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Pred. No. 2.7e-69;
1; Mismatches 2; Indels
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                           ISGF3 p91-related transcription factor - mouse
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illarity 98.7%;
Conservative
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Best Local Si
Matches 226;
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250 GPPNACLDQLQ--
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                            Cinconsion, was an englaced to the control of Approximated gene factor 3 pgl-related transpaces on the control of Approximated gene factor 3 pgl-related transpaces number: A54444 MUID:94208062; PMID:7512451
A; Accession: A54444
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-770 < RES>
A; Cross-references: UNIPROT:P40763; GB:L29277; NID:9475788; PID:9475789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Datesion: Add159
R;Schindler, C: Fu, X.Y.; Improta, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG
A;Reference number: A46159; MUID:92366557; PMID:1502203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 NHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIG 124
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Species: Homo sapiens (man)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NHPTAAVVTEKOOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 GNNQSVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                 A,Gene: GDB.STAT3; APRF
A,Cross-references: GDB.358950
A,Map position: 17421-17421
C,Superfamily: human signal transducer and transcription activator STATSA
C,Keywords: DNA binding; transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 VELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 739;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1152; DB 2;
Pred. No. 5.9e-69;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; not compared wit
A;Molecule type: nucleic acid; protein
Residues: 1-719 «SCH»
A;Cross-references: UNIPROT:P4224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.3%;
Matches 225; Conservative
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C;Accession: A56647
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
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A;Residues: 1-851 «YAN»
A;Residues: 1-851 «YAN»
A;Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; PID:g1293920
B;Cross-references: EMBL:U18671; Nen, Z.; Darnell Jr., J.E.
B;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-rrferences: UNIPROT:P42228; GB:U09351; NID:9509502; PIDN:AAA19692.1; PID:950950 C;Superfamily: human signal transducer and transcription activator STAT5A C;Keywords: DNA binding; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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-- QVRQQLKKLEELEQKYTYEHDPITKNKQVLWDRTFSLF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 PLHNGLDQLQNCFTLLAESLFQLRQQLEKLQEQSTKMTYEGDPIPAQRAHLLERATFLIY 309
                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 VTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKS--QGDMQDLNGNNQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 VTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 748;
                                                                                gamma-interferon activation site-binding protein Stat4 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66; Indels
                                                  185 RNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cuery Match
Best Local Similarity 45.5%; Pred. No. 2.8e-26;
Matches 102; Conservative 48; Mismatches 64
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A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:248538; NID:g758633; PIDN:CAA8 R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L. Proco. Natl. Acad. Sci. US.A. 92; 8831-8835, 1995 A;Fitle: Cloning and expression of Stats and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleuki A;Reference number: S54772; MUID:95237198; PMID:7720707 A;Accession: S54772 A;Accession: S54772 A;Accession: S54772 A;Status: preliminary; nucleic acid sequence not shown
                                                                                        254 QWKRRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRAEHLCQQLPIPG-PVEEM 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.7 RMSRETALGÓKQVSLETWLQREAGTLGÓYRVELAEKHQKTLGLLRKGÓTIILDDELIGWK 256
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                                                                                                                                                                                                                                                                  194 PQERMSRETALQQKQVSLETWLQREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDDBLI 253
                                                                                                                                                                                                                                                                                                                                           113 DWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 RRPEIACIGGPPNICLDRLENWITSLAESQLOTROQIKKLEELQOKVSYKGDPIVQHRPM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: stat5 protein
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54772; 14927; 14927;
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and
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C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
                                              AAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNY-KTLKSQGDMQDLNGNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 LAEVNATITDIISALVTSTFIIEKQP------PQVLKTQTKFAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 RPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 LEERIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLV 224
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Pred. No. 2.2e-10;
1; Mismatches 97; Indels
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A;Molecule type: mRNA
A;Residues: 1-793 <RES>
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30.6%;
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Best Local Similarity 30.6%
Best Local Conservative
70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammary gland factor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-793 <MUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: 149273
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A;Roteule type: mRNA
A;Residues: 1-786 < RES>
A;Cross-references: UNIPROT: Q9JKM1; EMBL: U21110; NID: G747973; PIDN: AAC52
B;Mu1, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A;Reference number: S54773
A;Accession: S54773
A;Accession: S54773
A;Reidues: Preliminary; nucleic acid sequence not shown
A;Reidues: 1-432, E', 434-786 < MUI>A;Reidues: 1-432, E', 434-786 < MUI>A;Reidues: 1-432, E', 434-786 < MUI>A;Reidues: 1-432, E', 434-786 < MUI>A;Coss-references: EMBL: Z48539; NID: G758635; PIDN: CAA88420.1; PID: G758636
A;Cross-reference number: S54727
A;Accession: S54727
A;Accession: S54727
A;Accession: S54727
A;Accession: S54727
A;Accession: S54725; MUID: 95246733; PMID: 7537213
A;Accession: S54727
A;Accession: S64725
A;Accession: A;Accession: A;Accession:
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149274; S54773; S54727
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved A;Reference number: 149273; MUID:96004632; PMID:7568026
                                      A,Accession: S53873
A,Status: nucleic acid sequence not shown
A,Status: nucleic acid sequence not shown
A,Molecule type: DNA
A,Residues: 1-196;392-591;884-730 <YAW>
A,Fross-references: EMBL:U18671
C,Generics:
A,Gene: stat2
A,Gene: stat2
A,Generics: 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2;
C,Superfamily: human signal transducer and transcription activator STATSA
C;Keywords: signal transduction; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 DHGLEQLETWFTAGAKLLFHLRQLLKELKGLSCLVSYQDDPLTKGVDLRNAQVTELLQRL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NICLDRIENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 VTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVT
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27.5%; Score 322; DB 2; Length 851;
Best Local Similarity 33.5%; Pred. No. 6.9e-14;
Matches 74; Conservative 51; Mismatches 90; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 MKSAFVVEROPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPE 228
Reference number: $53873; MUID:95192056; PMID:7885841
Accession: $53873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 22.9%; Score 268.5; DB 2; Similarity 30.6%; Pred. No. 2.2e-10; 71; Conservative 41; Mismatches 99;
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Matches 71; Conserv
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157557
DNA-Binding Protein and transcription factor - mouse
C;Species: Mus musculus (house mouse)
C;Species: May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 157557
S;Qualle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Clev Mol. Cell. Biol. 15, 3336-3343, 1995
A;Title: Cloning of murine State and human State, Stat proteins that are tyrosine phosp
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A;Cross-references: UNIPROT:P52633; GB:L47650; NID:gL008876; PIDN:AAA79006.1; PID:g1008
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Species: 128-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54740
R;Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 PLKLVAT----FROILOGKKKAV-----MEQFRHLPMPFHWKQEELKFKTGLRRLOHR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 NQSV--TRQKMQQ------LEQML-----TALDQMRRSIVSELAGLLSAMEYVQKTL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 TDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 D----LNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMBYVQKTLTDEELA 112
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A, Rossidues: Universes: Unive
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C;Superfamily: human signal transducer and transcription activator STATSA
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                                                176 LEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLV 224
                                                                                                 316 VNATITDIISALVTSTFIIEKQP------PQVLKTQTKFAATVRLLV 356
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             th 10.8%; Score 127; DB 2; Similarity 24.7%; Pred. No. 0.58; 59; Conservative 37; Mismatches 93;
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 59; Conserval
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A; Residues: 1-837 < RES>
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                                                                                                                                                                                                                                                       A,Molecule type: mRNA
A,Residues: 1-794 <LIN>
A,Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g115
C,Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: mRNA

A, Residues: 1-794 < WAKA.

A, Residues: 1-794 < WAKA.

A, Cross-references: UNIPROT: P42231; EMBL: X78428; NID: 9602354; PIDN: CAA55191.1; PID: 96023

A, Note: this is a revision to the sequence from reference S44353

R, Wakao, H.; Gonilleux, F.; Groner, B.

EMBO J. 13, 2182-2191, 1994

A, Title: Manmary gland factor (MGF) is a novel member of the cytokine regulated transcri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mammary gland factor - sheep

(Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

(Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

(Species: Ovis orientalis aries, Ovis ammon alies (species)

(Species: Ovis orientalis aries, Ovis ammon 03-Nov-1995 #text_change 09-Jul-2004

(Species: Orientalism, F.; Groner, B.

(SWakao, H.; Goulleux, F.; Groner, B.

(BMD OF 14, 884-855, 1855)

(A) Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula A; Reference number: 855527; MUD:95188889; PMID:7882987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 NGNNQSVTRQKMQQLEQML----TALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----QSVTRQKWQQLEQML----TALDQMRRSIVSELAGLLSAMEYVQXTLTDEELADWK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-71.6, RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STATSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 VTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNY-KTLKSQGDMQDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 LEERIVELFRNLMKSAFVVEROPCMPMHPDRPLVIKTGVOFTTKVRLLV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 VNATITDIISALVTSTFIIEKQP------POVLKTQTKRAATVRLLV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 794;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.4%; Score 262.5; DB 2; 30.1%; Pred. No. 5.6e-10; rative 42; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

20.2%; Score 237; DB 2;
Best Local Similarity 29.3%; Pred. No. 2.8e-08;
Matches 67; Conservative 41; Mismatches 99,
                                                                           Submitted to the EMBL Data Library, December 1995 Akeference number: H01043 Akeference number: H01043 Akecesion: G02317 Akecession: G02317 Akecession: preliminary; translated from GB/EMBL/DDBJ Akeres:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 69; Conserv
C; Accession: G02317
R; Lin, J.
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9

A; Gene: APE1216  Query Match Best Local Similarity 21.2%; Pred. No. 0.73; 6  Matches 42; Conservative 48; Mismatches 66; Indels 42;  Qy WIEKQOMLEQHLQDARKRVQDLEQKKVVENLQDDF	Db 379 LARAGASLEDLATRIDOVA-STICHCHIATATESTICALINE 1   1:1:1:1:1:1:1:1:1:1:1:1:1:1:1:1:1:1	13 (K.; Takah (aki, J.; K (aki, J.; K (aki
	RESULT 12 ABIGNT ABIGN ABIGN ABIGN C; Species: Nostoc sp. (strain PCC 7120) C; Species: Nostoc sp. PCC 7120 C; Species: Nostoc sp. Strain PCC 7120 C; Species: Nostoc sp. Strain PCC 7120 C; Sacession: AE1947 Nakazaki, N.; Sakamco, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Samura, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yamada, M.; Tabata, S. A; Reference number: AB1807; MUID:21595285; PMID:11759840 A; Recession: AE1947 A; Rocession: AE1947 A; Molecule type: DNA A; Scatus: preliminary A; Scatus: preliminary A; Scatus: preliminary A; Scatus: Prediminary A; Scatus: Procession: Rest Respection protein SWC1 C; Genetics: C; Superfamily: chromosome segregation protein SWC1 Query Match Ss; Conservative 47; Mismatches 76; Indels 49; Gaps 11; Matches 58; Conservative 47; Mismatches 76; Indels 49; Gaps 11; Best Local Similarity 25.2%; Pred: No. 1.7; Matches 58; Conservative 47; Mismatches 58; Conservative 58; SavyTexQQMCRQQREAPREARQQRIGENGARIANQQRICQRIANQQSRLGARIANGQRICGRIALDQWRRSIVGENGALIANDDRFD-FRYKTLK:	

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A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Acatus: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1166 < WIL>
A;Cross-references: EMBL:AL021497; PIDN:CAA16403.1; GSPDB:GN00023; CESP:Y51A2D.16
A;Experimental source: clone Y51A2D
A;Experimental source: clone Y51A2D
A;Gene: CESP:Y51A2D.16
A;Gene: CESP:Y51A2D.16
A;Map position: 5
A;Introns: 17/3; 45/1; 76/2; 156/3; 240/2; 288/2; 594/2; 657/3; 756/3; 798/2; 900/3; 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- 129
                                                                                                                                                                                                                                                                                                                                                                                                                      :: || :: | :: | :: | 488 LENDLKTCQTQLELES-------KKLQRLREDLVLEKSRRADLIGRIHSLCTTLSLN 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 FDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEY- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        538 GANFEKINNDDELIDNIDDIMMNALVAVKRERDDLRİQGNQQİQELHDLKRDIEKLRRSE 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 --CLDRLENWITSLAESQLQTRQQI----KKLEELQQKVSYKGDPIVQHRPMLEERIVEL 183
                                                                                                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQ----QMLEQHLQD------ARKRVQDLEQKMKVVENLQDD 42
                                                                                                                                                                                                                                                                                                                             72; Indels 73; Gaps
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 21.4%; Pred. No. 2.3;
Matches 52; Conservative 46; Mismatches 72; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 ---VOKTLTDEELAD-------WKRPEIACIGGPPNI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: May 25, 2005, 17:45:30 Job time: 22.6038 secs
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May 25, 2005, 17:15:30 ; Search time 95.284 Seconds (without alignments) 1230.701 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                            Run on:
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1 NHPTAAVVTEKQOMLEQHLQ.....IKTGVQFTTKVRLLVKFPEL 229 US-10-090-185-31 Perfect score: Scoring table: Sequence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** 

1612378 seqs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

																							,									
	Description	P40763 homo sapien	P42227 mus musculu	P52631 rattus norv	P61635 bos taurus	Q6dv79 gallus gall		Q7zxk3 xenopus lae	Q7zts5 brachydanio		Q6gue7 oryzias lat			Q90y16 tetraodon f	013133 oncorhynchu	Q9n145 macaca mula	Q8jgn0 xenopus lae	Q6p6q7 rattus norv	Q9qxk0 rattus norv	Q8c497 mus musculu	Q99k94 mus musculu	Q8c3v4 mus musculu	Q9d323 mus musculu	mus r	P42224 homo sapien	homo		P42225 mus musculu	O13131 oncorhynchu	Q8jfu8 brachydanio	Q704w6 bos taurus	093598 brachydanio
SUMMARIES	ID	STA3 HUMAN	STA3 MOUSE	STA3_RAT	STA3 BOVIN	Q6DV79	Q9PVX8	Q72XK3	Q7ZTS5	Q6DVF3	Q6GUE7	Q6NV46	093599	Q90Y16	013133	Q9N145	Q8JGN0	Q6P6Q7	оэрхко	Q8C497	Q99K94	Q8C3V4	Q9D323	Q8C8M3	STA1 HUMAN	Q68D00	Q764M5	STA1 MOUSE	013131	QBJFUB	Q704W6	093598
	DB	-	Н	Н	н	~	~	7	7	~	~	~	~	7	~	~	~	~	~	~	~	~	7	~		7	~	Н	7	~	~	7
	Query Match Length DB	770	770	770	770	771	769	166	414	765	785	786	908	764	767	163	751	712	749	749	712	749	749	755	750	750	757	749	754	528	108	749
مين	Query	98.7	98.7	98.5	98.1	96.6	93.8	93.5	86.3	86.3	86.3	86.3	86.3	84.2	83.4	56.0	49.1	48.9	48.9	48.7	48.6	48.6	48.6	48.6	48.5	48.5	48.5	48.0	46.1	45.5	45.4	45.4
	Score	1157	1157	1154	1150	1132	1099	1096	1011	1011	1011	101	1011	987	977	959	575	573	573	571	570	570	570	570	269	569	569	562	540.5	533	532.5	532
	Result No.	-	73	e	4	Ŋ	v	7	89	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

O6p943 brachydanio	Q801y2 carassius a	Q14765 homo sapien		Ol3132 oncorhynchu	Q8aw24 brachydanio	P42228 mus musculu	Q7zz53 brachydanio	Q8aw20 brachydanio	Q7zz77 brachydanio	Q8jfu7 brachydanio	Q66hb2 rattus norv	Q8jf85 brachydanio	Q90y15 tetraodon f	
Q6P943	Q801Y2	STA4 HUMAN	Q90 <u>Y</u> I7	013132	Q8AW24	STA4 MOUSE	Q722 <u>5</u> 3	QBAW20	07ZZ77	Q8JFU7	066нв2	QBJFS5	Q90Y15	
~	7	-	7	7	7	-	~	~	~	N	~	7	7	
749	718	748	758	754	657	749	651	667	652	553	748	1153	737	
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45	45	44.4	44	44	43	43	43	43	43	42	42	42.9	41	
532	531.5	520	519.5	517.5	513	504.5	504	504	503.5	503	503	503	491	-
32	33	34	35	36	37	38	39	40	41	42	43	44	45	,

## ALIGNMENTS

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TISSUBENCE FROM N.A. (ISOPORMS 1 AND DEL-701).

TISSUB-Kidney, and Pancreas;

MEDLINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A lacknil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,

A placknil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,

Hopkins R.P., Jordan H., Moore T., Max S.I., Haish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                  TISSUB=Placenta;
MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
Yoshida K., Sudo T., Naruto M., Kishimoto T.;
"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gpl30-mediated signaling
pathway:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
Rajkumar N., Yi Q., Nickerson D.A.;
"SeattleSNPs. NHLBI H46682 program for genomic applications, UW-
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1; Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.; "Highly conserved amino-acid sequence between murine STAT3 and a revised human STAT3 sequence."; Gene 213:119-124(1998).
                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
              GTA3 HUMAN STANDARD; PRT; 770 AA.
P40763; O14916; Q9BW54;
O1-F88-1995 (Rel. 31, Created)
05-UTL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                     Name=STAT3; Synonyms=APRF;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell 77:63-71(1994).
                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                  response factor)
STA3_HUMAN
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RESULT
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GO:0005634; C:nucleus; TAS.
GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pubmed=1173079; DOI=10.1074/jbc.M111486200; Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.; Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.; "Functional interaction of STAT3 transcription factor with the coactivator NoA/SRCIa.";
J. Biol. Chem. 277:8004-8011(2002)
-!- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6) responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOId=P40763-2; Sequence=VSP 010474;
TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
                                                                                                                                                                                                                                                                                                                                                                                            Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S., Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      muscle, kidney and pancreas.
-!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, ILF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimens and maximal transcriptional activity.
-!- SIMILARITY: Belongs to the transcription factor STAT family.
-!- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                      Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P40763-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                      [6]
PHOSPHORYLATION ON SERINE.
MEDLINE=95215843; PubMed=7701321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ012463; CAA10032.1; -. EMBL; AX572796; AAS66986.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC000627; AAH00627.1; -. EMBL; BC014482; AAH14482.1; -. EMBL; AF029311; AAB84254.1; -.
                                                                                                                                                                                                                         SEQUENCE OF 564-704 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L29277; AAA58374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 267:1990-1994(1995)
                                                                                                                                                   and mouse cDNA sequences."
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HGNC:11364; STAT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H-InvDB; HIX0013840; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH NCOAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Del-701;
                                                                                                                                                                                                                                                IISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P42227
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9
                                                                  . .; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 NHPTAAVVTEKQOMLEQHLODVRKRVQDLEQKMKVVENLQDDFDFDFNYKTLKSQGDMQDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                InterPro; 1PKUU121, 1 Pfau Pfau; 1 Pfau; PF0017; SH2, 1 laba; 1.
Pfam; PF02864; STAT laba; 1.
Pfam; PF02865; STAT lab; 1.
Pfam; PF02865; STAT lat; 1.
PROSITE; PS50001; SH2; 1.
Activator; Alternative splicing; DNA-binding; Nuclear protein; Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
Phosphorylation; Polymorphism; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
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MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 response factor).

Name-Stat3; Synonyws=Aprf;

Name-stat3; Synonyws=Aprf;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last amnotation update)
signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                    transcription from P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1157; DB 1; Length 770; Pred. No. 2.9e-65;
                                                                                                                                                                                                                                                                                                                                                                                                      Phosphoserine (By similarity)
Missing (in isoform Del-701).
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Q -> K (in dbSNP:1803125).
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GO, GO:0003700; F:transcription factor activity; TAS.
GO; GO:0006928; P:cell motility; TAS.
GO; GO:0001229; P:JAK-STAT cascade; TAS.
GO; GO:000122; P:Description of transcription
GO; GO:0001399; P:negative regulation of transcription
GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:00071899; P:signal transduction; TAS.
InterPro; IPR000890; FS3_like_DNA_bnd.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q -> H (in Ref. 1).
P -> S (in Ref. 1).
K -> N (in Ref. 1).
Y -> Y (in Ref. 1).
T -> A (in Ref. 1).
T -> A (in Ref. 1).
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Matches 226; Conservative
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770 AA;
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727
701
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P42227;
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SECURATE FOOR NAT. (120) CERT STAIRS).

STRAIN=FVB/N; TISSUE=Wammary gland;
MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B.B., Buctow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
D. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,
A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. M. Madan A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                        MEDLINE=95014185; PubMed=7523373;
Raz R., Durbin J.E., Levy D.E.;
"Acute phase response factor and additional members of the interferonstimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395 (1994).
Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T.; "Molecular cloning of ARRF, a novel IRW-stimulated gene factor 3 p91-related transcription factor involved in the gpl30-mediated signaling
                                                                                                                                                Zhong Z., Wen Z., Darnell J.E. Jr., "Stat3: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6."; science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM STAT3B).
STRAIN=BALB/c, and CS7BL/6; TISSUR=Liver;
MEDLINE=96016116; PubMed=7560809;
Schaefer T.S., Sanders L.K., Nathans D.;
"Cooperative transcriptional activity of Jun and Stat3 beta, a short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structure of the mouse stat 3/5 locus: evolution from Drosophila to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/G, and NOD/Ltd.
Davoodi-Semiromi A., She J.-X.;
Davoodi-Semiromi A., She J.-X.;
A mutant StatSb with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=129/SvJ;
PubMed=11161808; DOI=10.1006/geno.2000.6433;
Miyoshi K., Cui Y., Riedlinger G., Lehoczky J., Zon L., Oka T.,
Dewar K., Hennighausen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                       SEQUENCE FROM N.A. (ISOFORM STAT3A).
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                                                                                                                                    MEDLINE=94188718; PubMed=8140422;
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                                                                           Cell 77:63-71(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                               form of Stat3.";
                                                                                                                         TISSUE=Thymus;
                                                                                                                                                                                                                                               TISSUE=Brain;
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MRDLINESSISTOR, Pubmed-13.E. Jr.;

Wenz Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zhong Z., Zh
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                                          Phosphotyrosine (by JAK) (By similarity).
                                                        TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
FDMDLTSECATSPM -> FIDAVWK (in isoform
                                                                                                                                                                                                                                                                                                     1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
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                                                                                           /FTId=VSP_010475.
S->A: Decreased transcriptional
     PROSITE; PS50001; SH2; 1.
3D-structure; Activator; Acute phase; Alternative splicing;
Direct protein sequencing; DNA-binding; Nuclear protein;
                                                                                   Missing (In isoform Del-701)
                     2; Indels
                                                                                                               -> K (in Ref. 2).
-> T (in Ref. 2 and 4).
-> I (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Signal transducer and activator of transcription 3.
                                                                                                                                                                                                                                                                       Query Match
98.7%; Score 1157; DB 1;
Best Local Similarity 98.7%; Pred. No. 2.9e-65;
Matches 226; Conservative 1; Mismatches 2
                                                                             FTId=VSP 006287
                                                Phosphoserine
                                                                                                        activation.
E -> K (in F
S -> T (in F
M -> I (in F
                                                                       Stat3B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
25-OCT-2004 (Rel. 45, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                Name=Stat3;
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P52631;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on itse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.sib.ch).
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                                                                                                                                                                                                                                                                                                  nuclei late in an acute phase response and bind interleukin-6 response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACUTE - Phase protein genes.

PATHWAY: Involved in the gp130-mediated signaling pathway.

PATHWAY: Involved in the gp130-mediated signaling pathway.

SUBNIT: Forms a homodimer or a heterodimer with a related family member (at least STATI). Interacts with NCOAI (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).

FTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity (By similarity).

SIMILARITY: Belongs to the transcription factor STAT family.
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J. Biol. Chem. 270:29998-30006(1995).
-!- FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLN
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Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                      "Transcription factors Stat3 and Stat5b are present in rat liver
MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29999;
Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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HSSP; P42227; 1BG1.
RGD; J772; Stat3.
InterPro; IPR008967; P53 like_DNA_bnd.
InterPro; IPR001217; STAT.
Pfan; PF001017; STAT.
Pfan; PF01017; STAT_alpha; 1.
Pfan; PF02865; STAT_alpha; 1.
Pfan; PF02865; STAT_int; 1.
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RESULT 6
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                                                                                                                                                                                                                                                    TISSUE-Mammary gland;

A Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;

The STATSB-encoding gene was flipped across the STAT3/STAT5A-locus
The STATSB-encoding gene was flipped across the STAT3/STAT5A-locus
The State of the intervent of the intervent of the interleukin-6

- FUNCTION: Transcription factor that binds to the interleukin-6

- FUNCTION: Transcription factor that binds to the interleukin-6

- I.E. of the intervent of the intervent of various acute-phase protein genes (By similarity).

- PATHWAY: Involved in the gpl30-mediated signaling pathway.

- SUBURITY: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).

- SUBCELLUTAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).

- SIMILARITY: Belongs to the transcription factor STAT family.
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Phosphoserine (By similarity).
9CEB147C73E83274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50001; SH2; 1.
Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
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                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
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                                                              05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-GTA and activator of transcription 3.
Name=STAT3;
                770 AA
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                PRT;
                                                  (Rel. 44, Created)
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Matches 225; Conservative
                STANDARD;
                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=9913;
                BOVIN
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771 AA

PRELIMINARY;

Q6DV79; Q6DV79; RESULT S Q6DV79 ID Q6DV AC Q6DV

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191 NNQSVTRQKMQQLEQMLTALDQMRRGIVSELAGLLSAMEYVQKMLADEELADWKRRQQIA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 HPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNG
                                                                      Signal transducer and activator of transcription 3.
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognethae, Galliformes, Phasianidae, Phasianinae,
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"Activation of Stat3 by cytokine receptor gpl30 ventralizes Xenopus embryos independent of BMP-4.";
Dev. Biol. 216.481-490(1999).
EMBL; AB017701; BAA86061.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SLOUGH G.Y., Leung F.C.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AX641397; AAT64887.1; -.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004871; F:signal transcuber activity; IEA.

GO; GO:000742; P:transcription factor activity; IEA.

GO; GO:000755; P:transcription factor activity; IEA.

GO; GO:000535; P:transcription of transcription, DNA-dependent; IEA.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88174 MW; 71AC855C5DEC03E2 CRC64;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1132; DB 2;
Pred. No. 1.1e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           769 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR008967; Ps3_like_DNA_bnd.
InterPro, IPR000980; SH2.
InterPro, IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00017; SH2; 1.
Pfam; PF01017; SH2; 1.
Pfam; PF01864; STAT alpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT bint; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 221; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=stat 3;
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"Generation and initial analysis of more than 15,000 full-length human
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Last annotation update)
                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                       Klein S., Strausberg R.;
Submitted (JAN-2003) to the
EMBL; BC044717; AAH44717.1;
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01.JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, Stat3 protein.
                                                                                                                                                                Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 91.7
Matches 210; Conservative
                  mouse cDNA sequences
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                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                          SEQUENCE FROM N.A.
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NCBI_TaxID=7955;
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Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Brownstein M.J., Usdin T.B., Tonaldo M.F., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Boomstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Munny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hy,

Raha S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Munny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hy,

Raha S., Modan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

N. Jones S.J., Marra M.A.;
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                                                                                                                                                                                                                                                                                     Gaps
         GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001980; SH2.
InterPro; IPR001317; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                   Score 1099; DB 2; Length 7
Pred. No. 1.4e-61;
9; Mismatches 8; Indels
                                                                                                                                                                                                                      769 AA; 87974 MW; 0905C03263303069 CRC64;
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Last annotation update)
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Pfam; PF01017; STAT_alpha; 1.
Pfam; PF02864; STAT_bind; 1.
Pfam; PF02865; STAT_int; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                     93.8%;
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SEQUENCE
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Q7ZXK3;
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DR GO; GO:0005634; C:nucleus; IEA.

CO; GO:0005634; C:nucleus; IEA.

CO; GO:0005634; C:nucleus; IEA.

CO; GO:00005634; C:nucleus; IEA.

CO; GO:0007242; P:signal transcutcur activity; IEA.

CO; GO:0007242; P:intracellular signaling cascade; IEA.

CO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000990; SH2.

R Pfam; PF0017; STAT alpha; 1.

Pfam; PF0017; STAT alpha; 1.

Pfam; PF02864; STAT bind; 1.

Pfam; PF02865; STAT int; 1.

R SMART; SM00252; STAT int; 1.

R ROSITE; PS50001; SH2; 1.

R ROSITE; PS50001; SH2; 1.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Query Match
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,
Alusner R.D., Collins F.S., Wagner L., Shaefer C.F., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
Abtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M. J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Scheilutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation factor 3.
25-OCT-2004 (Madaka fish) (Japanese ricefish).
26-OCT-2004 (Madaka fish) (Japanese ricefish).
27-OCT-2004 (Madaka fish) (Japanese ricefish).
28-OCT-2004 (TrEMBLrel) (Japanese ricefish).
28-OCT-2004 (TrEMBLrel) (Japanese ricefish).
29-OCT-2004 (TrEMBLrel) (Japanese ricefish).
30-OCT-2004 (TrEMBLrel) (Japanese ricefish).
30-OCT-2004 (TrEMBLrel) (Japanese ricefish).
31-OCT-2004 (TrEMBLrel) (TrEMBLrel) (Japanese ricefish).
31-OCT-2004 (TrEMBLrel) (TrEMBLrel) (TrEMBLRel) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (TrEMBLREL) (Tr
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008967; P53 like_DNA_bnd.
InterPro; IPR001217; STAT.
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fam; PF02064; STAT_bind; 1.
fam; PF02065; STAT_int; 1.
EQUENCE 414 AA; 48253 MW; 0FFD1B509B7526BD CRC64;
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STRAIN=AB; TISSUE=Whole body;
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Submitted (JAN-2003) to the
EMBL; BC045276; AAH45276.1;
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."
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190 GINSQAAATRQKWAQLEQMLSALDQLRRQIVTEMGGLLTAMDYVQKNLTDEELADWKRRQQ 249
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
07-Jule annotation a isoform 1.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracciption factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX641434; AAT46364.1; -
GO, GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0007427; P:irranscription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009867; P53_like_DNA_bnd.
InterPro; IPR00980; STAT.
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Acanthomorpha; Acanthopterygii; Percomórpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias
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84.8%; Pred. No. 5.2e-56;
ive 19; Mismatches 14;
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InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
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Pfam; PF01017; STAT allpha; 1.
Pfam; PF02864; STAT bind; 1.
Pfam; PF02865; STAT_int; 1.
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Pfam; PF01017; STAT_alpha; 1.
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SEQUENCE 765 AA; 87
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SEQUENCE FROM N.A.
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PRELIMINARY;
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                                                                                                                                                   786 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=stat3;
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                                                                                                                                                 SEQUENCE
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WEDISUE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

A litschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A pitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toobliyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcha A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rywinski M.I., Skalska U., Smailus D.E., Schnerch A., Sothein J.E.,

A nones S.J., Marra M.A.,

A nones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                             5
                                                                                                                                   GNNQ-SVTRQKWQQLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRRPE 119
                                                                                                                                                                                                                                IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                          250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIKKLEELQQKVSYKGDPIIQHRPALEEK 309
                                                                                                                        9
                                                                                                                     HPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955,
                                                                                                                                                                                                                                                                                  180 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                    310 IVDLFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTNKVRLLVKFPEL 359
                                                                                             7
                                                              Ouery Match 86.3%; Score 1011; DB 2; Length 785; Best Local Similarity 84.8%; Pred. No. 5.3e-56; Matches 195; Conservative 19; Mismatches 14; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC068320; ABC068320.1; --
ZFIN; ZDB-087NE-980526-68; stat3.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
                                 89643 MW; 81F231BDB27DB938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=stat3;
Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                            Q6NV46;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Pfam; PF02864; STAT_bind; 1.
            Pfam, PF02865; STAT int; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 785 AA; 89643 MW
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stat3 protein.
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                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                190 GNSQAAATRQKMSQLEQMLSALDQLRRQIVTEMAGLLSAMDFVQKNLTDEELADWKRRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                            GNNQ-SVTRQKWQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR008967; P32 like DNA_bnd.
InterPro; IPR001217; STAT.
Pfam; PF0017; STAT.
Pfam; PF0017; STAT alpha; 1.
Pfam; PF02864; STAT lint; 1.
Pfam; PF02865; STAT lint; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 IVDLFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 359
                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                Length 786;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 IVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL
                                                                                                                                                                                                                                                                                                      13; Indels
                                                                                                                                                                                                                     90039 MW; FC7371D0B0E5447E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74BC4EA401C3C942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                              Query Match
86.3%; Score 1011; DB 2;
Best Local Similarity 84.8%; Pred. No. 5.4e-56;
Matches 195; Conservative 20; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.3%; Score 1011; DB 2; 84.8%; Pred. No. 5.5e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50001; SH2; 1.
806 AA; 92151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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Name=rbtStat3;
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  RESULT 14
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                               GNNQ-SVTROKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
                                                                                                        IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                     250 IACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPIIQHRPALEEK 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                          HPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 HPTAAVVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
 Gaps
                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neoperygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes; Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P4227; 18G1.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004871; F:signal transducer activity; IEA.

GO; GO:000710; F:signal transducer activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

Fram; PF00107; STAT albha; 1.

Pfam; PF01017; STAT alpha; 1.

Pfam; PF02864; STAT int; 1.
 2,
                                                                                                                                                IVELFRNIAMKSAFVVERQPCAMPAHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Indels
                                                                                                                                                                                                                                                                                                                                                                               Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF307106; AAL09415.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E661FFE18BEFD8BE CRC64;
                                                                                                                                                                                                                                                                        Last annotation update)
13;
                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.2%; Score 987; DB 2;
83.5%; Pred. No. 1.7e-54;
                                                                                                                                                                                                                             764 AA.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Mismatches
                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                           Tetraodon fluviatilis (Puffer fish)
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87411 MW;
                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 192; Conservative
                                                                                                                                                                                                                            PRELIMINARY;
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PROSITE; PS50001; SF
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=47145;
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Matches
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60 NGNNQ-SVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 QIACIGGPPKICLDRLETWITSLGBIQLQIRQOIKKLBELQQKVSYKGDPIIQHRPALEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 EIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NHPTAAVVTEKQQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDM-QDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                      Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 RIVELFRNIMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPEL 229
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                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:000370; F:transcription factor activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Signal transducer and activator of transcription (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Johnson M.C., Mourich D.V., Leong J.C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
EMBL, 160333, AAB60926.1; -.
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Arredondo J.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008967; P53 like_DNA_bnd.
InterPro; IPR001909; SH2_
InterPro; IPR01217; STAT.
Pfam; PF01017; STAT alpha; 1.
Pfam; PF0264; STAT blnd; 1.
Pfam; PF02655; STAT blnd; 1.
SEQUENCE 767 AA; 87816 MW; PED97740C74C3798 CRC64;
                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 977; DB 2;
; Pred. No. 7.4e-54;
24; Mismatches 17;
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                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.4*
Matches 188; Conservative
                                      01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                             NCBI_TaxID=8022;
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             R HSSP; P42227; 1861.

R GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.

GO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR001217; STAT.

R Pfam; PF01017; STAT. alpha; 1.

R Pfam; PF02064; STAT_alpha; 1.

R Pfam; PF02064; STAT_alpha; 1.

T NON TER.

1 100N TER.

1 163 163

Q SEQÜENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;
                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                               Query Match 56.0%; Score 656; DB 2; Length 163; Best Local Similarity 98.4%; Pred. No. 3.1e-34; Matches 126; Conservative 1; Mismatches 1; Indels
EMBL; AF227560; AAF73401.1; -.
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